

Val	Ile	Ser	Asp	Pro	Ala	Asp	Pro	Arg	Leu	Asp	Asp	Val	Arg	Asp	Leu	
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aac	cat	tcc	gat	tcc	cgg	cca	gac	cta	ccc	ggg	ggc	aaa	ggc	ctt	gtt	211
Asn	His	Ser	Asp	Ser	Arg	Pro	Asp	Leu	Pro	Gly	Gly	Lys	Gly	Leu	Val	
			25					30					35			
gtt	gcc	gaa	ggg	ccg	ttg	gtg	gtt	ggg	cgg	ctt	ctg	gaa	tcg	cgt	tac	259
Val	Ala	Glu	Gly	Pro	Leu	Val	Val	Gly	Arg	Leu	Leu	Glu	Ser	Arg	Tyr	
		40					45					50				
cca	gtg	cgt	gcg	atc	gtc	ggg	ttt	aaa	aac	aag	ctg	gat	tct	ttc	ctc	307
Pro	Val	Arg	Ala	Ile	Val	Gly	Phe	Lys	Asn	Lys	Leu	Asp	Ser	Phe	Leu	
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gac	agc	atc	gat	gca	tcc	ctt	gtt	gaa	ggc	atc	cca	gtg	tat	gag	gta	355
Asp	Ser	Ile	Asp	Ala	Ser	Leu	Val	Glu	Gly	Ile	Pro	Val	Tyr	Glu	Val	
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tcc	cgc	gag	ctc	ctc	gca	gag	gtc	gca	ggg	ttt	gat	atg	cac	cgc	gga	403
Ser	Arg	Glu	Leu	Leu	Ala	Glu	Val	Ala	Gly	Phe	Asp	Met	His	Arg	Gly	
			90						95					100		
ctt	ctg	gcg	aca	gcc	gat	cgc	acc	gag	gaa	gca	agt	gtt	gcg	cag	gtt	451
Leu	Leu	Ala	Thr	Ala	Asp	Arg	Thr	Glu	Glu	Ala	Ser	Val	Ala	Gln	Val	
			105					110					115			
cta	gaa	aac	gcc	cgc	acc	gtg	gtg	gtg	ctg	gaa	ggc	gta	ggc	gat	cac	499
Leu	Glu	Asn	Ala	Arg	Thr	Val	Val	Val	Leu	Glu	Gly	Val	Gly	Asp	His	
		120					125					130				
gaa	aac	atc	gga	tcc	atg	ttc	cgc	aac	gca	gca	ggc	atg	ggc	gtt	gac	547
Glu	Asn	Ile	Gly	Ser	Met	Phe	Arg	Asn	Ala	Ala	Gly	Met	Gly	Val	Asp	
	135					140					145					
gcc	atc	ttg	ttc	ggc	aac	ggg	tgt	gcc	gat	cct	ttg	tat	cga	cgt	gtc	595
Ala	Ile	Leu	Phe	Gly	Asn	Gly	Cys	Ala	Asp	Pro	Leu	Tyr	Arg	Arg	Val	
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gtt	cga	gtc	tca	atg	ggc	cac	gtg	ctc	cgc	ctg	ccg	ttc	gca	cac	ttg	643
Val	Arg	Val	Ser	Met	Gly	His	Val	Leu	Arg	Leu	Pro	Phe	Ala	His	Leu	
				170					175					180		
gaa	ggc	acc	tac	acc	acg	tgg	cag	cgc	agc	tta	gag	cag	ctc	aaa	gaa	691
Glu	Gly	Thr	Tyr	Thr	Thr	Trp	Gln	Arg	Ser	Leu	Glu	Gln	Leu	Lys	Glu	
			185					190					195			
gcc	gga	ttc	cac	ctc	gtt	tca	ctc	acc	cca	gat	cca	gag	gcg	gaa	cac	739
Ala	Gly	Phe	His	Leu	Val	Ser	Leu	Thr	Pro	Asp	Pro	Glu	Ala	Glu	His	
		200					205					210				
ctc	gaa	gat	gcg	ctc	gca	ggc	aaa	gac	aaa	gtg	gct	cta	ctc	gtg	ggc	787
Leu	Glu	Asp	Ala	Leu	Ala	Gly	Lys	Asp	Lys	Val	Ala	Leu	Leu	Val	Gly	
	215					220					225					
gct	gaa	ggc	cca	ggc	ctg	acc	gag	cat	gcg	atg	cgc	gcc	acc	gat	gtc	835
Ala	Glu	Gly	Pro	Gly	Leu	Thr	Glu	His	Ala	Met	Arg	Ala	Thr	Asp	Val	
230					235					240					245	
cgc	gcc	cgc	atc	ccg	atg	gcg	ccg	ggg	acc	gat	agc	ttg	aac	ctg	gct	883
Arg	Ala	Arg	Ile	Pro	Met	Ala	Pro	Gly	Thr	Asp	Ser	Leu	Asn	Leu	Ala	

250 255 260

acc tcg gcg gcg att gcg ttt tat gaa cgg gat cgc tca cag cgt 928
Thr Ser Ala Ala Ile Ala Phe Tyr Glu Arg Asp Arg Ser Gln Arg
265 270 275

taagtaacag cgctaagtag tag 951

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<213> Corynebacterium glutamicum

<400> 278

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Gly Lys Gly Leu Val Val Ala Glu Gly Pro Leu Val Val Gly Arg Leu
35 40 45

Leu Glu Ser Arg Tyr Pro Val Arg Ala Ile Val Gly Phe Lys Asn Lys
50 55 60

Leu Asp Ser Phe Leu Asp Ser Ile Asp Ala Ser Leu Val Glu Gly Ile
65 70 75 80

Pro Val Tyr Glu Val Ser Arg Glu Leu Leu Ala Glu Val Ala Gly Phe
85 90 95

Asp Met His Arg Gly Leu Leu Ala Thr Ala Asp Arg Thr Glu Glu Ala
100 105 110

Ser Val Ala Gln Val Leu Glu Asn Ala Arg Thr Val Val Val Leu Glu
115 120 125

Gly Val Gly Asp His Glu Asn Ile Gly Ser Met Phe Arg Asn Ala Ala
130 135 140

Gly Met Gly Val Asp Ala Ile Leu Phe Gly Asn Gly Cys Ala Asp Pro
145 150 155 160

Leu Tyr Arg Arg Val Val Arg Val Ser Met Gly His Val Leu Arg Leu
165 170 175

Pro Phe Ala His Leu Glu Gly Thr Tyr Thr Thr Trp Gln Arg Ser Leu
180 185 190

Glu Gln Leu Lys Glu Ala Gly Phe His Leu Val Ser Leu Thr Pro Asp
195 200 205

Pro Glu Ala Glu His Leu Glu Asp Ala Leu Ala Gly Lys Asp Lys Val
210 215 220

Ala Leu Leu Val Gly Ala Glu Gly Pro Gly Leu Thr Glu His Ala Met
225 230 235 240

Arg Ala Thr Asp Val Arg Ala Arg Ile Pro Met Ala Pro Gly Thr Asp

245

250

255

Ser Leu Asn Leu Ala Thr Ser Ala Ala Ile Ala Phe Tyr Glu Arg Asp
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Arg Ser Gln Arg
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<211> 666

<212> DNA

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aacgattcca ccggtattaa acattgctga aatagggcgg atg tgg gct cgt gac 115
 Met Trp Ala Arg Asp
 1 5

ata aac ttt cta tac atg agt aca gag cag gaa ctg caa atc gga aaa 163
 Ile Asn Phe Leu Tyr Met Ser Thr Glu Gln Glu Leu Gln Ile Gly Lys
 10 15 20

gtt gta aaa tcc cac ggc att cgg ggt gaa gtc gtg gtg gaa ttg agc 211
 Val Val Lys Ser His Gly Ile Arg Gly Glu Val Val Val Glu Leu Ser
 25 30 35

acc gat gat cca gac att cgc ttc gcc att ggg gaa gtt ctc aac ggc 259
 Thr Asp Asp Pro Asp Ile Arg Phe Ala Ile Gly Glu Val Leu Asn Gly
 40 45 50

aag cag gca ggc aag gag cat tca ctg acc atc gat gca gcg cgc atg 307
 Lys Gln Ala Gly Lys Glu His Ser Leu Thr Ile Asp Ala Ala Arg Met
 55 60 65

cac caa ggt cga ctc ttg gtg aag ttc gca gag gtc cca gat cgt acc 355
 His Gln Gly Arg Leu Leu Val Lys Phe Ala Glu Val Pro Asp Arg Thr
 70 75 80 85

gct gct gat tct ttg cgt gga act cga ttc ttt gcg gca cct ctt gag 403
 Ala Ala Asp Ser Leu Arg Gly Thr Arg Phe Phe Ala Ala Pro Leu Glu
 90 95 100

gat gaa gac gat gag gat ggc ttc tac gac cat gag ttg gaa ggt ctg 451
 Asp Glu Asp Asp Glu Asp Gly Phe Tyr Asp His Glu Leu Glu Gly Leu
 105 110 115

cgc gtc att cac gag ggc gag gat atc ggt gaa gtc acc ggc gtg atg 499
 Arg Val Ile His Glu Gly Glu Asp Ile Gly Glu Val Thr Gly Val Met
 120 125 130

cat ggc cca gcc ggt gag atc ctg gaa gtc cgc ctg acc tca ggc aag 547
 His Gly Pro Ala Gly Glu Ile Leu Glu Val Arg Leu Thr Ser Gly Lys
 135 140 145

gaa aca ctg att cct ttt gtg cac gcc att gtt cct gag gtg gat ctg 595
Glu Thr Leu Ile Pro Phe Val His Ala Ile Val Pro Glu Val Asp Leu
150 155 160 165

gaa gaa gga acc gca acg atc acc cct cca gag ggc ttg tta gat ctt 643
Glu Glu Gly Thr Ala Thr Ile Thr Pro Pro Glu Gly Leu Leu Asp Leu
170 175 180

taggctccga cagatttaat agt 666

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<213> Corynebacterium glutamicum

<400> 280

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20 25 30

Val Val Glu Leu Ser Thr Asp Asp Pro Asp Ile Arg Phe Ala Ile Gly
35 40 45

Glu Val Leu Asn Gly Lys Gln Ala Gly Lys Glu His Ser Leu Thr Ile
50 55 60

Asp Ala Ala Arg Met His Gln Gly Arg Leu Leu Val Lys Phe Ala Glu
65 70 75 80

Val Pro Asp Arg Thr Ala Ala Asp Ser Leu Arg Gly Thr Arg Phe Phe
85 90 95

Ala Ala Pro Leu Glu Asp Glu Asp Asp Glu Asp Gly Phe Tyr Asp His
100 105 110

Glu Leu Glu Gly Leu Arg Val Ile His Glu Gly Glu Asp Ile Gly Glu
115 120 125

Val Thr Gly Val Met His Gly Pro Ala Gly Glu Ile Leu Glu Val Arg
130 135 140

Leu Thr Ser Gly Lys Glu Thr Leu Ile Pro Phe Val His Ala Ile Val
145 150 155 160

Pro Glu Val Asp Leu Glu Glu Gly Thr Ala Thr Ile Thr Pro Pro Glu
165 170 175

Gly Leu Leu Asp Leu
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<212> DNA

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                                   Val Thr Pro Pro Ala
                                   1                               5

cgc cga gat ggc aca ccg gac aag aag cag agc aat cgc tct ggc gga 163
Arg Arg Asp Gly Thr Pro Asp Lys Lys Gln Ser Asn Arg Ser Gly Gly
                                   10                               20

tac cgg tct tca gtt cgt ggc tac aag cca gga tca tcc cgc cca aac 211
Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly Ser Ser Arg Pro Asn
                                   25                               30                               35

aca cgc cag cag cct cag aag aag gat gag att ctt ctc tcc aac gct 259
Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile Leu Leu Ser Asn Ala
                                   40                               45                               50

aag cct gcc aag aag caa aac gta aaa tcc gac gac gat tgg tcg atg 307
Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp Asp Asp Trp Ser Met
                                   55                               60                               65

ggg ttc tta aac cgc aat gac tct gac gga gtt cgc ctg cag aag gtg 355
Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val Arg Leu Gln Lys Val
                                   70                               75                               80                               85

ctt gcc caa gca ggt gtg gca tca cgt cga cac gca gaa atc ctg att 403
Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His Ala Glu Ile Leu Ile
                                   90                               95                               100

gat cag ggc cgt gtg gag gtc aac gat cgt atc gtg acc acc cag ggc 451
Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile Val Thr Thr Gln Gly
                                   105                               110                               115

gtg cgc gtg gat cca aac aac gat gtc atc cgt gtt gac ggc gtc cgc 499
Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg Val Asp Gly Val Arg
                                   120                               125                               130

atc cac atc aac gag gac ctc gag tac ttc gtg ctc aac aag cct cgt 547
Ile His Ile Asn Glu Asp Leu Glu Tyr Phe Val Leu Asn Lys Pro Arg
                                   135                               140                               145

ggc atg cac tcc acc atg agc gat gaa ctt ggt cgc cca tgc gtg ggt 595
Gly Met His Ser Thr Met Ser Asp Glu Leu Gly Arg Pro Cys Val Gly
                                   150                               155                               160                               165

gat ctg gtc agt gag aag act gca tct gga cag cgt ctg ttc cac gtc 643
Asp Leu Val Ser Glu Lys Thr Ala Ser Gly Gln Arg Leu Phe His Val
                                   170                               175                               180

ggg cgc ctc gac gcg gac acc gaa ggt ttg ctg ctg ctc acc aac gat 691
Gly Arg Leu Asp Ala Asp Thr Glu Gly Leu Leu Leu Leu Thr Asn Asp
                                   185                               190                               195

ggg gag ttg gct aac cgc ctc atg cac cct aag tac gaa gtg tcc aag 739
Gly Glu Leu Ala Asn Arg Leu Met His Pro Lys Tyr Glu Val Ser Lys

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200	205	210	
act tac ctt gct acc gtt cgc ggt gaa gca acc aat aag cta gtc agc			787
Thr Tyr Leu Ala Thr Val Arg Gly Glu Ala Thr Asn Lys Leu Val Ser			
215	220	225	
gct ctt cgt gat ggc gtg gag ttg gaa gat ggc cct gcc aag gct gac			835
Ala Leu Arg Asp Gly Val Glu Leu Glu Asp Gly Pro Ala Lys Ala Asp			
230	235	240	245
ttt gcg cag att atc gac gta ttc cag ggc aag tcc ttg ttg cgc atc			883
Phe Ala Gln Ile Ile Asp Val Phe Gln Gly Lys Ser Leu Leu Arg Ile			
250	255	260	
gaa atc cac gaa ggc cgc aag cac att gtg cga cgc ctc ttc gat gag			931
Glu Ile His Glu Gly Arg Lys His Ile Val Arg Arg Leu Phe Asp Glu			
265	270	275	
ctc ggt ttc cca gtc gag cgc ctc gtg cgc acc aag ctg cac acc gtt			979
Leu Gly Phe Pro Val Glu Arg Leu Val Arg Thr Lys Leu His Thr Val			
280	285	290	
cag ctt ggt gat cag aag cca ggt tcc ctt cgt gca ctg aac tcc tct			1027
Gln Leu Gly Asp Gln Lys Pro Gly Ser Leu Arg Ala Leu Asn Ser Ser			
295	300	305	
gag ctg acc agc tta tac aag gtg gtc caa ctg tgacggaaat ttccaacatg			1080
Glu Leu Thr Ser Leu Tyr Lys Val Val Gln Leu			
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cct			1083
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Asn Arg Ser Gly Gly Tyr Arg Ser Ser Val Arg Gly Tyr Lys Pro Gly			
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Ser Ser Arg Pro Asn Thr Arg Gln Gln Pro Gln Lys Lys Asp Glu Ile			
35	40	45	
Leu Leu Ser Asn Ala Lys Pro Ala Lys Lys Gln Asn Val Lys Ser Asp			
50	55	60	
Asp Asp Trp Ser Met Gly Phe Leu Asn Arg Asn Asp Ser Asp Gly Val			
65	70	75	80
Arg Leu Gln Lys Val Leu Ala Gln Ala Gly Val Ala Ser Arg Arg His			
85	90	95	
Ala Glu Ile Leu Ile Asp Gln Gly Arg Val Glu Val Asn Asp Arg Ile			
100	105	110	
Val Thr Thr Gln Gly Val Arg Val Asp Pro Asn Asn Asp Val Ile Arg			

115					120					125					
Val	Asp	Gly	Val	Arg	Ile	His	Ile	Asn	Glu	Asp	Leu	Glu	Tyr	Phe	Val
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Leu	Asn	Lys	Pro	Arg	Gly	Met	His	Ser	Thr	Met	Ser	Asp	Glu	Leu	Gly
145					150					155					160
Arg	Pro	Cys	Val	Gly	Asp	Leu	Val	Ser	Glu	Lys	Thr	Ala	Ser	Gly	Gln
				165					170					175	
Arg	Leu	Phe	His	Val	Gly	Arg	Leu	Asp	Ala	Asp	Thr	Glu	Gly	Leu	Leu
			180					185					190		
Leu	Leu	Thr	Asn	Asp	Gly	Glu	Leu	Ala	Asn	Arg	Leu	Met	His	Pro	Lys
		195					200					205			
Tyr	Glu	Val	Ser	Lys	Thr	Tyr	Leu	Ala	Thr	Val	Arg	Gly	Glu	Ala	Thr
	210					215					220				
Asn	Lys	Leu	Val	Ser	Ala	Leu	Arg	Asp	Gly	Val	Glu	Leu	Glu	Asp	Gly
225					230					235					240
Pro	Ala	Lys	Ala	Asp	Phe	Ala	Gln	Ile	Ile	Asp	Val	Phe	Gln	Gly	Lys
				245					250					255	
Ser	Leu	Leu	Arg	Ile	Glu	Ile	His	Glu	Gly	Arg	Lys	His	Ile	Val	Arg
			260					265					270		
Arg	Leu	Phe	Asp	Glu	Leu	Gly	Phe	Pro	Val	Glu	Arg	Leu	Val	Arg	Thr
		275					280					285			
Lys	Leu	His	Thr	Val	Gln	Leu	Gly	Asp	Gln	Lys	Pro	Gly	Ser	Leu	Arg
	290					295					300				
Ala	Leu	Asn	Ser	Ser	Glu	Leu	Thr	Ser	Leu	Tyr	Lys	Val	Val	Gln	Leu
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 <223> RXA02615

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 Met Gln Phe Ala Gln
 1 5
 aac ccg cgt ctg acg aac gac gcg gtg atc tta gaa cca ctg tca cat 163
 Asn Pro Arg Leu Thr Asn Asp Ala Val Ile Leu Glu Pro Leu Ser His

10										15					20					
cag	tgg	act	cag	gat	ctc	cag	gaa	gct	gtc	gcc	tca	caa	gaa	ttg	tgg	211				
Gln	Trp	Thr	Gln	Asp	Leu	Gln	Glu	Ala	Val	Ala	Ser	Gln	Glu	Leu	Trp					
25					30					35										
cgc	cat	tgg	ttc	gtc	gct	cta	ccc	acc	cca	gag	ggc	atg	gcg	gag	gaa	259				
Arg	His	Trp	Phe	Val	Ala	Leu	Pro	Thr	Pro	Glu	Gly	Met	Ala	Glu	Glu					
40			45					50												
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Ile	Asp	Arg	Arg	Leu	Ala	Glu	His	Ala	Asp	Gly	Leu	Cys	Ala	Pro	Trp					
55			60					65												
gca	atc	att	tcc	gct	gca	aca	ggc	cgt	gcc	gtt	ggc	atg	acc	tca	ttt	355				
Ala	Ile	Ile	Ser	Ala	Ala	Thr	Gly	Arg	Ala	Val	Gly	Met	Thr	Ser	Phe					
70	75					80					85									
cat	acc	ctt	gac	cac	gcg	aat	aaa	cgg	ctg	gaa	att	gga	cgc	aca	tgg	403				
His	Thr	Leu	Asp	His	Ala	Asn	Lys	Arg	Leu	Glu	Ile	Gly	Arg	Thr	Trp					
90					95					100										
atg	gct	gcc	cat	gtc	caa	gga	acc	ggc	atc	aac	ccc	tcg	gtg	aaa	ttc	451				
Met	Ala	Ala	His	Val	Gln	Gly	Thr	Gly	Ile	Asn	Pro	Ser	Val	Lys	Phe					
105				110					115											
ctg	cag	ttg	cag	cgc	gct	ttt	gaa	gac	ctc	ggg	gtc	aat	gcc	gtg	gaa	499				
Leu	Gln	Leu	Gln	Arg	Ala	Phe	Glu	Asp	Leu	Gly	Val	Asn	Ala	Val	Glu					
120			125					130												
ttc	cga	acg	aac	tgg	cac	aac	cac	cgc	tcc	cgc	gcc	gca	atc	gaa	cga	547				
Phe	Arg	Thr	Asn	Trp	His	Asn	His	Arg	Ser	Arg	Ala	Ala	Ile	Glu	Arg					
135			140					145												
ctc	gga	gca	aaa	caa	gac	ggc	gta	cta	cgc	aaa	cat	cgc	atc	cac	cct	595				
Leu	Gly	Ala	Lys	Gln	Asp	Gly	Val	Leu	Arg	Lys	His	Arg	Ile	His	Pro					
150	155					160					165									
gac	ggc	acc	gtc	cgc	gac	acc	gtc	atc	tat	tcc	atc	acc	aac	gat	gaa	643				
Asp	Gly	Thr	Val	Arg	Asp	Thr	Val	Ile	Tyr	Ser	Ile	Thr	Asn	Asp	Glu					
170					175					180										
tgg	cct	gcc	gtc	aaa	ctg	acg	ctc	atg	gag	cga	ctg	tac	cgt	cac	atg	691				
Trp	Pro	Ala	Val	Lys	Leu	Thr	Leu	Met	Glu	Arg	Leu	Tyr	Arg	His	Met					
185			190					195												
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Gln	Val	Pro	Ile	Ile	Pro	Asn	Glu	Ala	Ser	Leu	Phe	Asp	Ala	Ser						
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<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

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20 25 30

Ser Gln Glu Leu Trp Arg His Trp Phe Val Ala Leu Pro Thr Pro Glu
35 40 45

Gly Met Ala Glu Glu Ile Asp Arg Arg Leu Ala Glu His Ala Asp Gly
50 55 60

Leu Cys Ala Pro Trp Ala Ile Ile Ser Ala Ala Thr Gly Arg Ala Val
65 70 75 80

Gly Met Thr Ser Phe His Thr Leu Asp His Ala Asn Lys Arg Leu Glu
85 90 95

Ile Gly Arg Thr Trp Met Ala Ala His Val Gln Gly Thr Gly Ile Asn
100 105 110

Pro Ser Val Lys Phe Leu Gln Leu Gln Arg Ala Phe Glu Asp Leu Gly
115 120 125

Val Asn Ala Val Glu Phe Arg Thr Asn Trp His Asn His Arg Ser Arg
130 135 140

Ala Ala Ile Glu Arg Leu Gly Ala Lys Gln Asp Gly Val Leu Arg Lys
145 150 155 160

His Arg Ile His Pro Asp Gly Thr Val Arg Asp Thr Val Ile Tyr Ser
165 170 175

Ile Thr Asn Asp Glu Trp Pro Ala Val Lys Leu Thr Leu Met Glu Arg
180 185 190

Leu Tyr Arg His Met Gln Val Pro Ile Ile Pro Asn Glu Ala Ser Leu
195 200 205

Phe Asp Ala Ser
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Met Ser Lys Asn Ser
1 5

aag gcg tac cgc gag gcc gct gag aag atc gac gct ggt cgc atc tac 163
Lys Ala Tyr Arg Glu Ala Ala Glu Lys Ile Asp Ala Gly Arg Ile Tyr
10 15 20

tcc cca ctc gag gct gca aac ctg gtc aag gag acc tcc tcc aag aac 211
 Ser Pro Leu Glu Ala Ala Asn Leu Val Lys Glu Thr Ser Ser Lys Asn
 25 30 35

tac gac gct tcc atc gac gta gct atc cgc ctg ggc gtt gac cca cgt 259
 Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu Gly Val Asp Pro Arg
 40 45 50

aag gct gat cag ctt gtt cgt ggc acc gtc tcc ctg cct aac ggc acc 307
 Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser Leu Pro Asn Gly Thr
 55 60 65

ggt aag acc gtt cgc gtt gct gtg ttc gca cag ggc gag aag gct act 355
 Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln Gly Glu Lys Ala Thr
 70 75 80 85

gag gct gag gct gct ggc gct gac ttc gtt ggc acc gac gag ctc gtt 403
 Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly Thr Asp Glu Leu Val
 90 95 100

gag aag atc cag ggt ggc tgg acc gac ttc gac gtt gct att gca acc 451
 Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp Val Ala Ile Ala Thr
 105 110 115

cct gat cag atg gct aag atc ggc cgt atc gct cgt gtc ttg ggc cca 499
 Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala Arg Val Leu Gly Pro
 120 125 130

cgt ggt ctg atg cct aac cct aag acc ggc acc gtc acc aac gat gtc 547
 Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr Val Thr Asn Asp Val
 135 140 145

gct aag gct atc gaa gag gtc aag ggc ggc aag att tcc ttc cgc gtt 595
 Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys Ile Ser Phe Arg Val
 150 155 160 165

gac aag gct tcc aac ctg cac gct gca att ggt aag gct tcc ttc gat 643
 Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly Lys Ala Ser Phe Asp
 170 175 180

gcg aag aag ctg gct gag aac tac ggc gct ctc ctc gac gag atc atc 691
 Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu Leu Asp Glu Ile Ile
 185 190 195

cgt atc aag cct tct tcc gct aag ggc atc tac gtc aag cgc gtg acc 739
 Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr Val Lys Arg Val Thr
 200 205 210

ctg tct tcc acc acc ggt cct ggt gtt gag gtt gac act cac gtc acc 787
 Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val Asp Thr His Val Thr
 215 220 225

aag aac tac gca gaa gag gca taagccttcc cacgcgtaac tct 831
 Lys Asn Tyr Ala Glu Glu Ala
 230 235

<210> 286

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

Met Ser Lys Asn Ser Lys Ala Tyr Arg Glu Ala Ala Glu Lys Ile Asp
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Ala Gly Arg Ile Tyr Ser Pro Leu Glu Ala Ala Asn Leu Val Lys Glu
 20 25 30

Thr Ser Ser Lys Asn Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu
 35 40 45

Gly Val Asp Pro Arg Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser
 50 55 60

Leu Pro Asn Gly Thr Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln
 65 70 75 80

Gly Glu Lys Ala Thr Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly
 85 90 95

Thr Asp Glu Leu Val Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp
 100 105 110

Val Ala Ile Ala Thr Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala
 115 120 125

Arg Val Leu Gly Pro Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr
 130 135 140

Val Thr Asn Asp Val Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys
 145 150 155 160

Ile Ser Phe Arg Val Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly
 165 170 175

Lys Ala Ser Phe Asp Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu
 180 185 190

Leu Asp Glu Ile Ile Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr
 195 200 205

Val Lys Arg Val Thr Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val
 210 215 220

Asp Thr His Val Thr Lys Asn Tyr Ala Glu Glu Ala
 225 230 235

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<211> 674

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(651)

<223> FRXA01343

<400> 287

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aag	aac	tac	gac	gct	tcc	atc	gac	gta	gct	atc	cgc	ctg	ggc	gtt	gac	96	
Lys	Asn	Tyr	Asp	Ala	Ser	Ile	Asp	Val	Ala	Ile	Arg	Leu	Gly	Val	Asp		
			20					25					30				
cca	cgt	aag	gct	gat	cag	ctt	gtt	cgt	ggc	acc	gtc	tcc	ctg	cct	aac	144	
Pro	Arg	Lys	Ala	Asp	Gln	Leu	Val	Arg	Gly	Thr	Val	Ser	Leu	Pro	Asn		
			35				40					45					
ggc	acc	ggt	aag	acc	gtt	cgc	gtt	gct	gtg	ttc	gca	cag	ggc	gag	aag	192	
Gly	Thr	Gly	Lys	Thr	Val	Arg	Val	Ala	Val	Phe	Ala	Gln	Gly	Glu	Lys		
	50					55					60						
gct	act	gag	gct	gag	gct	gct	ggc	gct	gac	ttc	gtt	ggc	acc	gac	gag	240	
Ala	Thr	Glu	Ala	Glu	Ala	Ala	Gly	Ala	Asp	Phe	Val	Gly	Thr	Asp	Glu		
65					70				75						80		
ctc	gtt	gag	aag	atc	cag	ggt	ggc	tgg	acc	gac	ttc	gac	gtt	gct	att	288	
Leu	Val	Glu	Lys	Ile	Gln	Gly	Gly	Trp	Thr	Asp	Phe	Asp	Val	Ala	Ile		
				85					90					95			
gca	acc	cct	gat	cag	atg	gct	aag	atc	ggc	cgt	atc	gct	cgt	gtc	ttg	336	
Ala	Thr	Pro	Asp	Gln	Met	Ala	Lys	Ile	Gly	Arg	Ile	Ala	Arg	Val	Leu		
			100					105					110				
ggc	cca	cgt	ggt	ctg	atg	cct	aac	cct	aag	acc	ggc	acc	gtc	acc	aac	384	
Gly	Pro	Arg	Gly	Leu	Met	Pro	Asn	Pro	Lys	Thr	Gly	Thr	Val	Thr	Asn		
			115				120					125					
gat	gtc	gct	aag	gct	atc	gaa	gag	gtc	aag	ggc	ggc	aag	att	tcc	ttc	432	
Asp	Val	Ala	Lys	Ala	Ile	Glu	Glu	Val	Lys	Gly	Gly	Lys	Ile	Ser	Phe		
	130					135					140						
cgc	gtt	gac	aag	gct	tcc	aac	ctg	cac	gct	gca	att	ggt	aag	gct	tcc	480	
Arg	Val	Asp	Lys	Ala	Ser	Asn	Leu	His	Ala	Ala	Ile	Gly	Lys	Ala	Ser		
145					150					155					160		
ttc	gat	gcg	aag	aag	ctg	gct	gag	aac	tac	ggc	gct	ctc	ctc	gac	gag	528	
Phe	Asp	Ala	Lys	Lys	Leu	Ala	Glu	Asn	Tyr	Gly	Ala	Leu	Leu	Asp	Glu		
				165					170					175			
atc	atc	cgt	atc	aag	cct	tct	tcc	gct	aag	ggc	atc	tac	gtc	aag	cgc	576	
Ile	Ile	Arg	Ile	Lys	Pro	Ser	Ser	Ala	Lys	Gly	Ile	Tyr	Val	Lys	Arg		
			180					185					190				
gtg	acc	ctg	tct	tcc	acc	acc	ggt	cct	ggt	gtt	gag	gtt	gac	act	cac	624	
Val	Thr	Leu	Ser	Ser	Thr	Thr	Gly	Pro	Gly	Val	Glu	Val	Asp	Thr	His		
		195					200					205					
gtc	acc	aag	aac	tac	gca	gaa	gag	gca	taagccttcc	cacgcgtaac						671	
Val	Thr	Lys	Asn	Tyr	Ala	Glu	Glu	Ala									
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tct																674	

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<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

Ile Tyr Ser Pro Leu Glu Ala Ala Asn Leu Val Lys Glu Thr Ser Ser
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Lys Asn Tyr Asp Ala Ser Ile Asp Val Ala Ile Arg Leu Gly Val Asp
20 25 30

Pro Arg Lys Ala Asp Gln Leu Val Arg Gly Thr Val Ser Leu Pro Asn
35 40 45

Gly Thr Gly Lys Thr Val Arg Val Ala Val Phe Ala Gln Gly Glu Lys
50 55 60

Ala Thr Glu Ala Glu Ala Ala Gly Ala Asp Phe Val Gly Thr Asp Glu
65 70 75 80

Leu Val Glu Lys Ile Gln Gly Gly Trp Thr Asp Phe Asp Val Ala Ile
85 90 95

Ala Thr Pro Asp Gln Met Ala Lys Ile Gly Arg Ile Ala Arg Val Leu
100 105 110

Gly Pro Arg Gly Leu Met Pro Asn Pro Lys Thr Gly Thr Val Thr Asn
115 120 125

Asp Val Ala Lys Ala Ile Glu Glu Val Lys Gly Gly Lys Ile Ser Phe
130 135 140

Arg Val Asp Lys Ala Ser Asn Leu His Ala Ala Ile Gly Lys Ala Ser
145 150 155 160

Phe Asp Ala Lys Lys Leu Ala Glu Asn Tyr Gly Ala Leu Leu Asp Glu
165 170 175

Ile Ile Arg Ile Lys Pro Ser Ser Ala Lys Gly Ile Tyr Val Lys Arg
180 185 190

Val Thr Leu Ser Ser Thr Thr Gly Pro Gly Val Glu Val Asp Thr His
195 200 205

Val Thr Lys Asn Tyr Ala Glu Glu Ala
210 215

<210> 289

<211> 684

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(661)

<223> RXA01951

<400> 289

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cacatcgagt acgacccaaa ccgtaccgct aacattgcac ttg ctt cac tac ttc 115
Leu Leu His Tyr Phe

	1	5	
gat ggc gag aag cgt tac atc ctc gca ccg aag ggc ctg acc cag ggc			163
Asp Gly Glu Lys Arg Tyr Ile Leu Ala Pro Lys Gly Leu Thr Gln Gly			
	10	20	
acc gtt atc gag tcc ggc gct gca gcc gac atc aag gtt ggt aac aac			211
Thr Val Ile Glu Ser Gly Ala Ala Ala Asp Ile Lys Val Gly Asn Asn			
	25	30	35
ctg cca ctg cgt aac atc ccg act ggt acc acc atc cac aac gtg gag			259
Leu Pro Leu Arg Asn Ile Pro Thr Gly Thr Thr Ile His Asn Val Glu			
	40	45	50
ttg aag cca ggc gca ggt gca aag ctg gca cgt tcc gct gga gct tcc			307
Leu Lys Pro Gly Ala Gly Ala Lys Leu Ala Arg Ser Ala Gly Ala Ser			
	55	60	65
atc cag ctt ctt ggt aag gaa ggc tcc tac gca gtt ctg cgt atg cca			355
Ile Gln Leu Leu Gly Lys Glu Gly Ser Tyr Ala Val Leu Arg Met Pro			
	70	75	80
tcc tcc gag atc cga cgc gta aac atc cgc tgc cgc gcg act gtt ggt			403
Ser Ser Glu Ile Arg Arg Val Asn Ile Arg Cys Arg Ala Thr Val Gly			
	90	95	100
gag gtc ggc aac gcc gag cag atc aac att cgt tgg ggt aaa gct ggt			451
Glu Val Gly Asn Ala Glu Gln Ile Asn Ile Arg Trp Gly Lys Ala Gly			
	105	110	115
cgt atg cgt tgg aag ggc tgg cgc cca acc gtc cgt ggt gtc gtt atg			499
Arg Met Arg Trp Lys Gly Trp Arg Pro Thr Val Arg Gly Val Val Met			
	120	125	130
aac ccg gtc gac cac cca cac ggt ggt ggt gaa ggt aag act tct ggt			547
Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Lys Thr Ser Gly			
	135	140	145
ggt cgc cac cca gtc tcc cca tgg gga cag aag gaa ggc cgc acc cgc			595
Gly Arg His Pro Val Ser Pro Trp Gly Gln Lys Glu Gly Arg Thr Arg			
	150	155	160
aag cct aag cgt tac agc gat gac atg atc gtt cgt cgc cgt cgt gct			643
Lys Pro Lys Arg Tyr Ser Asp Asp Met Ile Val Arg Arg Arg Arg Ala			
	170	175	180
aac aag aac aag aag cgt taagaggagg taacggtgaa tgt			684
Asn Lys Asn Lys Lys Arg			
	185		

<210> 290

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

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Gly	Leu	Thr	Gln	Gly	Thr	Val	Ile	Glu	Ser	Gly	Ala	Ala	Ala	Asp	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20					25					30					
Lys	Val	Gly	Asn	Asn	Leu	Pro	Leu	Arg	Asn	Ile	Pro	Thr	Gly	Thr	Thr
		35					40					45			
Ile	His	Asn	Val	Glu	Leu	Lys	Pro	Gly	Ala	Gly	Ala	Lys	Leu	Ala	Arg
	50					55					60				
Ser	Ala	Gly	Ala	Ser	Ile	Gln	Leu	Leu	Gly	Lys	Glu	Gly	Ser	Tyr	Ala
	65				70					75					80
Val	Leu	Arg	Met	Pro	Ser	Ser	Glu	Ile	Arg	Arg	Val	Asn	Ile	Arg	Cys
				85					90					95	
Arg	Ala	Thr	Val	Gly	Glu	Val	Gly	Asn	Ala	Glu	Gln	Ile	Asn	Ile	Arg
			100					105					110		
Trp	Gly	Lys	Ala	Gly	Arg	Met	Arg	Trp	Lys	Gly	Trp	Arg	Pro	Thr	Val
		115					120					125			
Arg	Gly	Val	Val	Met	Asn	Pro	Val	Asp	His	Pro	His	Gly	Gly	Gly	Glu
	130					135					140				
Gly	Lys	Thr	Ser	Gly	Gly	Arg	His	Pro	Val	Ser	Pro	Trp	Gly	Gln	Lys
	145				150					155					160
Glu	Gly	Arg	Thr	Arg	Lys	Pro	Lys	Arg	Tyr	Ser	Asp	Asp	Met	Ile	Val
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Arg	Arg	Arg	Arg	Ala	Asn	Lys	Asn	Lys	Lys	Arg					
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> FRXA01950

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 cggtccgctc gcttaagacg tcgatagaaa aggacacatt atg gct att cgt aag 115
 Met Ala Ile Arg Lys 5
 tac aag ccg aca acc ccg ggt cgc cgc gca agc tcc gtt tcc atg ttc 163
 Tyr Lys Pro Thr Thr Pro Gly Arg Arg Ala Ser Ser Val Ser Met Phe 20
 acg gag atc acc cgt tcg acc cct gag aag tca ctt ctc cgc cca ctg 211
 Thr Glu Ile Thr Arg Ser Thr Pro Glu Lys Ser Leu Leu Arg Pro Leu 35
 agc aag acc ggc gga cgt aac tct cac ggc cac atc acc acc cgt cac 259
 Ser Lys Thr Gly Gly Arg Asn Ser His Gly His Ile Thr Thr Arg His 50

cgc ggt ggt gga cac aag cgc cgc tac cgc gtc atc gac ttc cgt cgt 307
Arg Gly Gly Gly His Lys Arg Arg Tyr Arg Val Ile Asp Phe Arg Arg
55 60 65

aac gac aag gat ggc gta ttg gca aag gtc gct cac atc gag tac gac 355
Asn Asp Lys Asp Gly Val Leu Ala Lys Val Ala His Ile Glu Tyr Asp
70 75 80 85

cca aac cgt acc gct aac att gca ctt gct tca cta ctt cga tgg cga 403
Pro Asn Arg Thr Ala Asn Ile Ala Leu Ala Ser Leu Leu Arg Trp Arg
90 95 100

gaa gcg tta cat cct cgc acc gaa ggg cct gac cca ggg cac cgt tat 451
Glu Ala Leu His Pro Arg Thr Glu Gly Pro Asp Pro Gly His Arg Tyr
105 110 115

cga gtc cgg cgc tgc agc cga cat caa ggt tgg taacaacctg ccactgcgta 504
Arg Val Arg Arg Cys Ser Arg His Gln Gly Trp
120 125

aca

507

<210> 292

<211> 128

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

Met Ala Ile Arg Lys Tyr Lys Pro Thr Thr Pro Gly Arg Arg Ala Ser
1 5 10 15

Ser Val Ser Met Phe Thr Glu Ile Thr Arg Ser Thr Pro Glu Lys Ser
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Leu Leu Arg Pro Leu Ser Lys Thr Gly Gly Arg Asn Ser His Gly His
35 40 45

Ile Thr Thr Arg His Arg Gly Gly Gly His Lys Arg Arg Tyr Arg Val
50 55 60

Ile Asp Phe Arg Arg Asn Asp Lys Asp Gly Val Leu Ala Lys Val Ala
65 70 75 80

His Ile Glu Tyr Asp Pro Asn Arg Thr Ala Asn Ile Ala Leu Ala Ser
85 90 95

Leu Leu Arg Trp Arg Glu Ala Leu His Pro Arg Thr Glu Gly Pro Asp
100 105 110

Pro Gly His Arg Tyr Arg Val Arg Arg Cys Ser Arg His Gln Gly Trp
115 120 125

<210> 293

<211> 777

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(754)

<223> RXA01286

<400> 293

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Met Ser Glu Asn Glu
1 5
atc aag ggc att ctg ggc acc aag ctc ggc atg act cag atc ttc gac 163
Ile Lys Gly Ile Leu Gly Thr Lys Leu Gly Met Thr Gln Ile Phe Asp
10 15 20
gag gag aac cgc gtt att ccg gtt acc gtc gtt gaa gcg ggt cca tgc 211
Glu Glu Asn Arg Val Ile Pro Val Thr Val Val Glu Ala Gly Pro Cys
25 30 35
gta gtt tcc cag att cgc acc gtt gag acc gat ggc tac aac gcc atc 259
Val Val Ser Gln Ile Arg Thr Val Glu Thr Asp Gly Tyr Asn Ala Ile
40 45 50
cag atc gcc tac ggc gaa atc gac cca cgc aag gtg aac cag cca ttg 307
Gln Ile Ala Tyr Gly Glu Ile Asp Pro Arg Lys Val Asn Gln Pro Leu
55 60 65
act ggt cac ttc aag aaa gca ggc gtt acc ccc cgc cgc cac gtc acc 355
Thr Gly His Phe Lys Lys Ala Gly Val Thr Pro Arg Arg His Val Thr
70 75 80 85
gag att cgt atg gac gat gtc tcc ggt tac gag gtt gga cag gac gtt 403
Glu Ile Arg Met Asp Asp Val Ser Gly Tyr Glu Val Gly Gln Asp Val
90 95 100
acc gtt gaa atc ttc aac gac atc aag ttc gtt gac gtc acc ggt acc 451
Thr Val Glu Ile Phe Asn Asp Ile Lys Phe Val Asp Val Thr Gly Thr
105 110 115
acc aag ggt aag ggc tac gcc ggc gct atg aag cgc cat ggc ttc gct 499
Thr Lys Gly Lys Gly Tyr Ala Gly Ala Met Lys Arg His Gly Phe Ala
120 125 130
ggc cag ggt gcc ggc cac ggt aac cag gct gca cac cgc cgc gta ggt 547
Gly Gln Gly Ala Gly His Gly Asn Gln Ala Ala His Arg Arg Val Gly
135 140 145
ggc att ggt gca gct gct acc cca ggt cgc atc ttc aag ggc aag cgt 595
Gly Ile Gly Ala Ala Ala Thr Pro Gly Arg Ile Phe Lys Gly Lys Arg
150 155 160 165
atg gct ggc cgc atg ggt aat gac cgc gtc acc acc cag aac ctc aag 643
Met Ala Gly Arg Met Gly Asn Asp Arg Val Thr Thr Gln Asn Leu Lys
170 175 180
gtt cag aag att gac gcc gat gcc aac atc atc ctt atc aag ggc gca 691
Val Gln Lys Ile Asp Ala Asp Ala Asn Ile Ile Leu Ile Lys Gly Ala
185 190 195

atc cct ggt aac cgt ggt ggc atc gtt acc gtt aag acc gca gtg aag 739
Ile Pro Gly Asn Arg Gly Gly Ile Val Thr Val Lys Thr Ala Val Lys
200 205 210

ggc ggt gca cac gca tgacgaatct gaagctgtat gtt 777
Gly Gly Ala His Ala
215

<210> 294
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 294
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20 25 30
Glu Ala Gly Pro Cys Val Val Ser Gln Ile Arg Thr Val Glu Thr Asp
35 40 45
Gly Tyr Asn Ala Ile Gln Ile Ala Tyr Gly Glu Ile Asp Pro Arg Lys
50 55 60
Val Asn Gln Pro Leu Thr Gly His Phe Lys Lys Ala Gly Val Thr Pro
65 70 75 80
Arg Arg His Val Thr Glu Ile Arg Met Asp Asp Val Ser Gly Tyr Glu
85 90 95
Val Gly Gln Asp Val Thr Val Glu Ile Phe Asn Asp Ile Lys Phe Val
100 105 110
Asp Val Thr Gly Thr Thr Lys Gly Lys Gly Tyr Ala Gly Ala Met Lys
115 120 125
Arg His Gly Phe Ala Gly Gln Gly Ala Gly His Gly Asn Gln Ala Ala
130 135 140
His Arg Arg Val Gly Gly Ile Gly Ala Ala Ala Thr Pro Gly Arg Ile
145 150 155 160
Phe Lys Gly Lys Arg Met Ala Gly Arg Met Gly Asn Asp Arg Val Thr
165 170 175
Thr Gln Asn Leu Lys Val Gln Lys Ile Asp Ala Asp Ala Asn Ile Ile
180 185 190
Leu Ile Lys Gly Ala Ile Pro Gly Asn Arg Gly Gly Ile Val Thr Val
195 200 205
Lys Thr Ala Val Lys Gly Gly Ala His Ala
210 215

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<211> 626

<212> DNA

<213> Corynebacterium glutamicum

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<222> (1)..(603)

<223> RXA01948

<400> 295

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ctg ctg cac cag gtt gtc aac gca cag ctt gca gca gct cga cag ggc	96
Leu Leu His Gln Val Val Asn Ala Gln Leu Ala Ala Ala Arg Gln Gly	
20 25 30	
acc cac tcc acc aag acc cgt ggc gaa gta cgt ggc ggt ggc cgt aag	144
Thr His Ser Thr Lys Thr Arg Gly Glu Val Arg Gly Gly Gly Arg Lys	
35 40 45	
cca ttc cgt cag aag gga acc ggt cgc gct cgt cag ggc tcg atc cgc	192
Pro Phe Arg Gln Lys Gly Thr Gly Arg Ala Arg Gln Gly Ser Ile Arg	
50 55 60	
gca cct cac ttc acc ggt ggt ggc atc tcc cac ggc cct aag cca cgc	240
Ala Pro His Phe Thr Gly Gly Gly Ile Ser His Gly Pro Lys Pro Arg	
65 70 75 80	
gac tac tct cag cgc acc cct aag aag atg atc aag gct gca ctt tac	288
Asp Tyr Ser Gln Arg Thr Pro Lys Lys Met Ile Lys Ala Ala Leu Tyr	
85 90 95	
ggt gca ctg tct gat cgt gca cgc aat gca cgt atc cac gtc gtc tcc	336
Gly Ala Leu Ser Asp Arg Ala Arg Asn Ala Arg Ile His Val Val Ser	
100 105 110	
gaa ttg gtg cct ggc cag acc cct tcg acc aag tct gca aag gct ttc	384
Glu Leu Val Pro Gly Gln Thr Pro Ser Thr Lys Ser Ala Lys Ala Phe	
115 120 125	
atc gag cgt ctg acc gag cgt aag tcc gtg ctg ctc gta gtg agc cgt	432
Ile Glu Arg Leu Thr Glu Arg Lys Ser Val Leu Leu Val Val Ser Arg	
130 135 140	
gag gat atc aac gcc cag aag agt gct aac aac ctg cct ggc gtc cac	480
Glu Asp Ile Asn Ala Gln Lys Ser Ala Asn Asn Leu Pro Gly Val His	
145 150 155 160	
atc ctg gcc gct gat cag ctg aac acc tac gac gtt ctc aag tct gac	528
Ile Leu Ala Ala Asp Gln Leu Asn Thr Tyr Asp Val Leu Lys Ser Asp	
165 170 175	
gac gtt gtg ttc tcc gtt gag gct ctc cac acc ttc atc aac cgc gct	576
Asp Val Val Phe Ser Val Glu Ala Leu His Thr Phe Ile Asn Arg Ala	
180 185 190	
tcc ggt gcg gca cag gag gag cag aac taatggctac tatcgccaac	623
Ser Gly Ala Ala Gln Glu Glu Gln Asn	
195 200	

cca

626

<210> 296
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 296
Ser Val Glu Leu Pro Ala Glu Ile Phe Asp Arg Glu Val Ser Val Ala
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20 25 30
Thr His Ser Thr Lys Thr Arg Gly Glu Val Arg Gly Gly Gly Arg Lys
35 40 45
Pro Phe Arg Gln Lys Gly Thr Gly Arg Ala Arg Gln Gly Ser Ile Arg
50 55 60
Ala Pro His Phe Thr Gly Gly Gly Ile Ser His Gly Pro Lys Pro Arg
65 70 75 80
Asp Tyr Ser Gln Arg Thr Pro Lys Lys Met Ile Lys Ala Ala Leu Tyr
85 90 95
Gly Ala Leu Ser Asp Arg Ala Arg Asn Ala Arg Ile His Val Val Ser
100 105 110
Glu Leu Val Pro Gly Gln Thr Pro Ser Thr Lys Ser Ala Lys Ala Phe
115 120 125
Ile Glu Arg Leu Thr Glu Arg Lys Ser Val Leu Leu Val Val Ser Arg
130 135 140
Glu Asp Ile Asn Ala Gln Lys Ser Ala Asn Asn Leu Pro Gly Val His
145 150 155 160
Ile Leu Ala Ala Asp Gln Leu Asn Thr Tyr Asp Val Leu Lys Ser Asp
165 170 175
Asp Val Val Phe Ser Val Glu Ala Leu His Thr Phe Ile Asn Arg Ala
180 185 190
Ser Gly Ala Ala Gln Glu Glu Gln Asn
195 200

<210> 297
<211> 696
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(673)
<223> RXN00706

<400> 297
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              Met Thr Glu Asn Tyr
              1                      5

atc cct cgt ctg aag acc cgt tac cag gac gaa atc cgc acc aag ctt 163
Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu Ile Arg Thr Lys Leu
              10                      15                      20

cag ggc gag ttc gag ttc gaa aac gtc atg cag atc cca ggc gtc acc 211
Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln Ile Pro Gly Val Thr
              25                      30                      35

aag att gtc gtc aac atg ggt gtc ggc gac gca gct cgt gac tcc aag 259
Lys Ile Val Val Asn Met Gly Val Gly Asp Ala Ala Arg Asp Ser Lys
              40                      45                      50

ctc atc aac ggc gct atc gag gac ctc acc gca atc acc ggt cag aag 307
Leu Ile Asn Gly Ala Ile Glu Asp Leu Thr Ala Ile Thr Gly Gln Lys
              55                      60                      65

cca cag ctt cgc cgt gcg aag aag tcc atc gct aac ttc aag ctc cgt 355
Pro Gln Leu Arg Arg Ala Lys Lys Ser Ile Ala Asn Phe Lys Leu Arg
              70                      75                      80                      85

gaa ggc atg cca atc ggc gca aag gtt acc ctg cgc ggc gac cgc atg 403
Glu Gly Met Pro Ile Gly Ala Lys Val Thr Leu Arg Gly Asp Arg Met
              90                      95                      100

tgg gag ttc ctg gac cgt ctg ctg acc gtg gca ctg cca cgt atc cgc 451
Trp Glu Phe Leu Asp Arg Leu Leu Thr Val Ala Leu Pro Arg Ile Arg
              105                      110                      115

gac ttc cgt gga ctt tcc gac cag cag ttc gac ggc cac ggt aac tac 499
Asp Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp Gly His Gly Asn Tyr
              120                      125                      130

acc ttc ggc ctc acc gag cag acc atg ttc tac gaa atc gac gtc gac 547
Thr Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr Glu Ile Asp Val Asp
              135                      140                      145

aag atc gac cgt cct cgt ggt atg gac atc acc gtt gtt acc acc gct 595
Lys Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala
              150                      155                      160                      165

gta acc gac gat gaa ggt cgc tcc ctg ctc cgc gag ctc ggc ttc cca 643
Val Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg Glu Leu Gly Phe Pro
              170                      175                      180

ttc aag ggt gaa gac ggc aac cgc cag cag taaactgcat agttaaaagc 693
Phe Lys Gly Glu Asp Gly Asn Arg Gln Gln
              185                      190

act 696

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<210> 298

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

Met Thr Glu Asn Tyr Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu
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 Ile Arg Thr Lys Leu Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln
 20 25 30
 Ile Pro Gly Val Thr Lys Ile Val Val Asn Met Gly Val Gly Asp Ala
 35 40 45
 Ala Arg Asp Ser Lys Leu Ile Asn Gly Ala Ile Glu Asp Leu Thr Ala
 50 55 60
 Ile Thr Gly Gln Lys Pro Gln Leu Arg Arg Ala Lys Lys Ser Ile Ala
 65 70 75 80
 Asn Phe Lys Leu Arg Glu Gly Met Pro Ile Gly Ala Lys Val Thr Leu
 85 90 95
 Arg Gly Asp Arg Met Trp Glu Phe Leu Asp Arg Leu Leu Thr Val Ala
 100 105 110
 Leu Pro Arg Ile Arg Asp Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp
 115 120 125
 Gly His Gly Asn Tyr Thr Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr
 130 135 140
 Glu Ile Asp Val Asp Lys Ile Asp Arg Pro Arg Gly Met Asp Ile Thr
 145 150 155 160
 Val Val Thr Thr Ala Val Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg
 165 170 175
 Glu Leu Gly Phe Pro Phe Lys Gly Glu Asp Gly Asn Arg Gln Gln
 180 185 190

<210> 299

<211> 256

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(256)

<223> FRXA00711

<400> 299

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 agaaggtccg cgtttctcgt cgcaatggga aggatatcta atg act gag aat tac 115
 Met Thr Glu Asn Tyr
 1 5
 atc cct cgt ctg aag acc cgt tac cag gac gaa atc cgc acc aag ctt 163
 Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu Ile Arg Thr Lys Leu
 10 15 20
 cag ggc gag ttc gag ttc gaa aac gtc atg cag atc cca ggc gtc acc 211
 Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln Ile Pro Gly Val Thr

25

30

35

aag att gtc gtc aac atg ggt gtc ggc gac gca gct cgt gac tcc 256
 Lys Ile Val Val Asn Met Gly Val Gly Asp Ala Ala Arg Asp Ser
 40 45 50

<210> 300

<211> 52

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

Met Thr Glu Asn Tyr Ile Pro Arg Leu Lys Thr Arg Tyr Gln Asp Glu
 1 5 10 15

Ile Arg Thr Lys Leu Gln Gly Glu Phe Glu Phe Glu Asn Val Met Gln
 20 25 30

Ile Pro Gly Val Thr Lys Ile Val Val Asn Met Gly Val Gly Asp Ala
 35 40 45

Ala Arg Asp Ser
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<210> 301

<211> 290

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(267)

<223> FRXA00706

<400> 301

gag ttc ctg gac cgt ctg ctg acc gtg gca ctg cca cgt atc cgc gac 48
 Glu Phe Leu Asp Arg Leu Leu Thr Val Ala Leu Pro Arg Ile Arg Asp
 1 5 10 15

ttc cgt gga ctt tcc gac cag cag ttc gac ggc cac ggt aac tac acc 96
 Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp Gly His Gly Asn Tyr Thr
 20 25 30

ttc ggc ctc acc gag cag acc atg ttc tac gaa atc gac gtc gac aag 144
 Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr Glu Ile Asp Val Asp Lys
 35 40 45

atc gac cgt cct cgt ggt atg gac atc acc gtt gtt acc acc gct gta 192
 Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala Val
 50 55 60

acc gac gat gaa ggt cgc tcc ctg ctc cgc gag ctc ggc ttc cca ttc 240
 Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg Glu Leu Gly Phe Pro Phe
 65 70 75 80

aag ggt gaa gac ggc aac cgc cag cag taaactgcat agttaaagc 287
 Lys Gly Glu Asp Gly Asn Arg Gln Gln
 85

act

290

<210> 302
 <211> 89
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 302
 Glu Phe Leu Asp Arg Leu Leu Thr Val Ala Leu Pro Arg Ile Arg Asp
 1 5 10 15
 Phe Arg Gly Leu Ser Asp Gln Gln Phe Asp Gly His Gly Asn Tyr Thr
 20 25 30
 Phe Gly Leu Thr Glu Gln Thr Met Phe Tyr Glu Ile Asp Val Asp Lys
 35 40 45
 Ile Asp Arg Pro Arg Gly Met Asp Ile Thr Val Val Thr Thr Ala Val
 50 55 60
 Thr Asp Asp Glu Gly Arg Ser Leu Leu Arg Glu Leu Gly Phe Pro Phe
 65 70 75 80
 Lys Gly Glu Asp Gly Asn Arg Gln Gln
 85

<210> 303
 <211> 657
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(634)
 <223> RXA00695

<400> 303
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 gtcctcgcct acgtctggtg atagggagga ttgactaaat atg tca cgt atc gga 115
 Met Ser Arg Ile Gly
 1 5
 aaa gaa ccg atc acc atc cca tcc ggt gtc gaa acc aag att gac gga 163
 Lys Glu Pro Ile Thr Ile Pro Ser Gly Val Glu Thr Lys Ile Asp Gly
 10 15 20
 cag ctc gtt gag gtt aag ggt cct aag ggc acc ctg aac gtt aac gtt 211
 Gln Leu Val Glu Val Lys Gly Pro Lys Gly Thr Leu Asn Val Asn Val
 25 30 35
 cca gag cca atc tcc gtt gca gtg gaa gac ggc aag att gtc gtc acc 259
 Pro Glu Pro Ile Ser Val Ala Val Glu Asp Gly Lys Ile Val Val Thr
 40 45 50
 cgc ccg gat gat cac cgc act aac cgt tcc ctc cac ggt ctc tcc cgc 307
 Arg Pro Asp Asp His Arg Thr Asn Arg Ser Leu His Gly Leu Ser Arg
 55 60 65

tcc ctg gtt aac aac ctg gtt gtc ggc gtc acc gag ggc tac acc atc 355
 Ser Leu Val Asn Asn Leu Val Val Gly Val Thr Glu Gly Tyr Thr Ile
 70 75 80 85

aag atg gaa atc ttc ggt gtc ggt tac cgt gtc gcg ctg aag ggc aag 403
 Lys Met Glu Ile Phe Gly Val Gly Tyr Arg Val Ala Leu Lys Gly Lys
 90 95 100

gac ctt gag ttc tcc ctc ggc tac tca cac cca gtt ctg att gaa gct 451
 Asp Leu Glu Phe Ser Leu Gly Tyr Ser His Pro Val Leu Ile Glu Ala
 105 110 115

tct gaa ggc atc act ttc gca gtt gat ggc aac acc aag ctt tca gtt 499
 Ser Glu Gly Ile Thr Phe Ala Val Asp Gly Asn Thr Lys Leu Ser Val
 120 125 130

tct ggc atc gac aag cag aag gtt gga cag gtc gca gca gtg atc cgc 547
 Ser Gly Ile Asp Lys Gln Lys Val Gly Gln Val Ala Ala Val Ile Arg
 135 140 145

cgc ctg cgt aag gac gat cct tac aag ggt aag ggc atc cgc tac gag 595
 Arg Leu Arg Lys Asp Asp Pro Tyr Lys Gly Lys Gly Ile Arg Tyr Glu
 150 155 160 165

ggt gag cag atc cgc cgc aag gtc gga aag acg ggt aag taagcaatga 644
 Gly Glu Gln Ile Arg Arg Lys Val Gly Lys Thr Gly Lys
 170 175

gcaacactga aaa 657

<210> 304

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

Met Ser Arg Ile Gly Lys Glu Pro Ile Thr Ile Pro Ser Gly Val Glu
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Thr Lys Ile Asp Gly Gln Leu Val Glu Val Lys Gly Pro Lys Gly Thr
 20 25 30

Leu Asn Val Asn Val Pro Glu Pro Ile Ser Val Ala Val Glu Asp Gly
 35 40 45

Lys Ile Val Val Thr Arg Pro Asp Asp His Arg Thr Asn Arg Ser Leu
 50 55 60

His Gly Leu Ser Arg Ser Leu Val Asn Asn Leu Val Val Gly Val Thr
 65 70 75 80

Glu Gly Tyr Thr Ile Lys Met Glu Ile Phe Gly Val Gly Tyr Arg Val
 85 90 95

Ala Leu Lys Gly Lys Asp Leu Glu Phe Ser Leu Gly Tyr Ser His Pro
 100 105 110

Val Leu Ile Glu Ala Ser Glu Gly Ile Thr Phe Ala Val Asp Gly Asn
 115 120 125

Thr Lys Leu Ser Val Ser Gly Ile Asp Lys Gln Lys Val Gly Gln Val
130 135 140

Ala Ala Val Ile Arg Arg Leu Arg Lys Asp Asp Pro Tyr Lys Gly Lys
145 150 155 160

Gly Ile Arg Tyr Glu Gly Glu Gln Ile Arg Arg Lys Val Gly Lys Thr
165 170 175

Gly Lys

<210> 305

<211> 549

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(526)

<223> RXA00543

<400> 305

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aacattcaca aacactcaaa aaccacgaaa ggcagggatc atg aag ctg atc ctc 115
Met Lys Leu Ile Leu
1 5

acc gcc gcc gtt gaa aac ctt ggt gtc gct ggc gac atc gta gag gtt 163
Thr Ala Ala Val Glu Asn Leu Gly Val Ala Gly Asp Ile Val Glu Val
10 15 20

aag aac ggc tac gga cgt aac ctg ctg ctc ccc cgt ggc ctg gca atc 211
Lys Asn Gly Tyr Gly Arg Asn Leu Leu Leu Pro Arg Gly Leu Ala Ile
25 30 35

gta gcc acc ccg ggt gct gag aag cag atc gag ggc atc aag cgt gcc 259
Val Ala Thr Pro Gly Ala Glu Lys Gln Ile Glu Gly Ile Lys Arg Ala
40 45 50

cag gag gct cgc gag att cgc gac ctc gac cac gct cgc gaa gtt aag 307
Gln Glu Ala Arg Glu Ile Arg Asp Leu Asp His Ala Arg Glu Val Lys
55 60 65

gta gca ctg gaa gca ctt gaa ggt gtt acc att gca gtc cgc acc tcc 355
Val Ala Leu Glu Ala Leu Glu Gly Val Thr Ile Ala Val Arg Thr Ser
70 75 80 85

gag agc gga aaa ctg ttc ggc tcc gtt aag act gac gac atc gtc gac 403
Glu Ser Gly Lys Leu Phe Gly Ser Val Lys Thr Asp Asp Ile Val Asp
90 95 100

gca gtc aag gca gcc ggc ggc ccg aac ctg gac aag cgt gcc att gtt 451
Ala Val Lys Ala Ala Gly Gly Pro Asn Leu Asp Lys Arg Ala Ile Val
105 110 115

ctc ccg aag aac ctg gtt aag acc acc ggt aag tac cag gta gaa gca 499
Leu Pro Lys Asn Leu Val Lys Thr Thr Gly Lys Tyr Gln Val Glu Ala
120 125 130

aag ctc acc gac gga att gtt tcc gcg tgaagtttga ggtcgtcgca 546
 Lys Leu Thr Asp Gly Ile Val Ser Ala
 135 140

gcg 549

<210> 306
 <211> 142
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 306
 Met Lys Leu Ile Leu Thr Ala Ala Val Glu Asn Leu Gly Val Ala Gly
 1 5 10 15
 Asp Ile Val Glu Val Lys Asn Gly Tyr Gly Arg Asn Leu Leu Leu Pro
 20 25 30
 Arg Gly Leu Ala Ile Val Ala Thr Pro Gly Ala Glu Lys Gln Ile Glu
 35 40 45
 Gly Ile Lys Arg Ala Gln Glu Ala Arg Glu Ile Arg Asp Leu Asp His
 50 55 60
 Ala Arg Glu Val Lys Val Ala Leu Glu Ala Leu Glu Gly Val Thr Ile
 65 70 75 80
 Ala Val Arg Thr Ser Glu Ser Gly Lys Leu Phe Gly Ser Val Lys Thr
 85 90 95
 Asp Asp Ile Val Asp Ala Val Lys Ala Ala Gly Gly Pro Asn Leu Asp
 100 105 110
 Lys Arg Ala Ile Val Leu Pro Lys Asn Leu Val Lys Thr Thr Gly Lys
 115 120 125
 Tyr Gln Val Glu Ala Lys Leu Thr Asp Gly Ile Val Ser Ala
 130 135 140

<210> 307
 <211> 636
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(613)
 <223> RXA01335

<400> 307
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 cggatcagta gattacacat aagaggaagg aggcgaagta atg gca aac cca aga 115
 Met Ala Asn Pro Arg
 1 5
 aac gaa gca gct ctg gca gag ctc aag gca cgt ttc gct gag acc gac 163
 Asn Glu Ala Ala Leu Ala Glu Leu Lys Ala Arg Phe Ala Glu Thr Asp

10										15					20					
acc gtc gtt ctc acc gag tac cgt ggc ctg acc gtg gct cag acc acc	211																			
Thr Val Val Leu Thr Glu Tyr Arg Gly Leu Thr Val Ala Gln Thr Thr																				
25 30 35																				
gaa ctg cgt aag gca ctg ggc ttc gat gtc cag tac tcc gtc gcc aag	259																			
Glu Leu Arg Lys Ala Leu Gly Phe Asp Val Gln Tyr Ser Val Ala Lys																				
40 45 50																				
aac acc ctt gtt aag atc gcc gct aac gaa gct ggc gtc gag ggc ctt	307																			
Asn Thr Leu Val Lys Ile Ala Ala Asn Glu Ala Gly Val Glu Gly Leu																				
55 60 65																				
gat gat ctc ctg acc ggt cca acc gct gtt gcc ttc atc aag ggc gaa	355																			
Asp Asp Leu Leu Thr Gly Pro Thr Ala Val Ala Phe Ile Lys Gly Glu																				
70 75 80 85																				
gca gtt gac acc gct aag gtg ctg aag aaa ttc ggc gaa gaa aac aag	403																			
Ala Val Asp Thr Ala Lys Val Leu Lys Lys Phe Gly Glu Glu Asn Lys																				
90 95 100																				
gca ttc gta gtc aag ggt ggc tac atg gat ggc aac gcg ctg acc gct	451																			
Ala Phe Val Val Lys Gly Gly Tyr Met Asp Gly Asn Ala Leu Thr Ala																				
105 110 115																				
gaa cag gtc aac gca atc gcc gag ctg gac aac cgt gag acc act ctc	499																			
Glu Gln Val Asn Ala Ile Ala Glu Leu Asp Asn Arg Glu Thr Thr Leu																				
120 125 130																				
gcg aag ctt gcc ggc gcc atg aag ggc agc ttg gca aag gcc gca ggc	547																			
Ala Lys Leu Ala Gly Ala Met Lys Gly Ser Leu Ala Lys Ala Ala Gly																				
135 140 145																				
ctg ttc aac gct cct gct tcc cag gtc gca cgc ctc gcc gtt gcg ctc	595																			
Leu Phe Asn Ala Pro Ala Ser Gln Val Ala Arg Leu Ala Val Ala Leu																				
150 155 160 165																				
cag gac aag aag gac gca taagtcgccca ccaggcgcac cag	636																			
Gln Asp Lys Lys Asp Ala																				
170																				

<210> 308

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 308

Met Ala Asn Pro Arg Asn Glu Ala Ala Leu Ala Glu Leu Lys Ala Arg	
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Phe Ala Glu Thr Asp Thr Val Val Leu Thr Glu Tyr Arg Gly Leu Thr	
20 25 30	
Val Ala Gln Thr Thr Glu Leu Arg Lys Ala Leu Gly Phe Asp Val Gln	
35 40 45	
Tyr Ser Val Ala Lys Asn Thr Leu Val Lys Ile Ala Ala Asn Glu Ala	
50 55 60	

Gly Val Glu Gly Leu Asp Asp Leu Leu Thr Gly Pro Thr Ala Val Ala
 65 70 75 80
 Phe Ile Lys Gly Glu Ala Val Asp Thr Ala Lys Val Leu Lys Lys Phe
 85 90 95
 Gly Glu Glu Asn Lys Ala Phe Val Val Lys Gly Gly Tyr Met Asp Gly
 100 105 110
 Asn Ala Leu Thr Ala Glu Gln Val Asn Ala Ile Ala Glu Leu Asp Asn
 115 120 125
 Arg Glu Thr Thr Leu Ala Lys Leu Ala Gly Ala Met Lys Gly Ser Leu
 130 135 140
 Ala Lys Ala Ala Gly Leu Phe Asn Ala Pro Ala Ser Gln Val Ala Arg
 145 150 155 160
 Leu Ala Val Ala Leu Gln Asp Lys Lys Asp Ala
 165 170

<210> 309
 <211> 558
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(535)
 <223> RXN02826

<400> 309
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 cgtcccagtt gtggccggtg acaaggaagc aggtttaacg atg gct cct aag aag 115
 Met Ala Pro Lys Lys
 1 5
 aag aag aag gtc act ggc ctc atc aag ctc cag atc cag gca gga cag 163
 Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln Ile Gln Ala Gly Gln
 10 15 20
 gca aac cct gct cct cca gtt ggc cca gca ctt ggt gct cac ggc gtc 211
 Ala Asn Pro Ala Pro Pro Val Gly Pro Ala Leu Gly Ala His Gly Val
 25 30 35
 aac atc atg gaa ttc tgc aag gct tac aac gct gcg act gaa aac cag 259
 Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala Ala Thr Glu Asn Gln
 40 45 50
 cgc ggc aac gtt gtt cct gtt gag atc acc gtt tac gaa gac cgt tca 307
 Arg Gly Asn Val Val Pro Val Glu Ile Thr Val Tyr Glu Asp Arg Ser
 55 60 65
 ttc gac ttc aag ctg aag act cct cca gct gca aag ctt ctt ctg aag 355
 Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala Lys Leu Leu Leu Lys
 70 75 80 85
 gct gct ggc ctg cag aag ggc tcc ggc gtt cct cac acc cag aag gtc 403
 Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro His Thr Gln Lys Val

90 95 100

ggc aag gtt tcc atg gct cag gtt cgt gag atc gct gag acc aag aag 451
Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile Ala Glu Thr Lys Lys
105 110 115

gaa gac ctg aac gct cgc gat atc gac gct gct gcg aag atc atc gct 499
Glu Asp Leu Asn Ala Arg Asp Ile Asp Ala Ala Ala Lys Ile Ile Ala
120 125 130

ggt acc gct cgt tcc atg ggc atc acc gtc gaa ggc taaaagcttt 545
Gly Thr Ala Arg Ser Met Gly Ile Thr Val Glu Gly
135 140 145

cacaccggtt agt 558

<210> 310
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 310
Met Ala Pro Lys Lys Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln
1 5 10 15
Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro Ala Leu
20 25 30
Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala
35 40 45
Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile Thr Val
50 55 60
Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala
65 70 75 80
Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro
85 90 95
His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile
100 105 110
Ala Glu Thr Lys Lys Glu Asp Leu Asn Ala Arg Asp Ile Asp Ala Ala
115 120 125
Ala Lys Ile Ile Ala Gly Thr Ala Arg Ser Met Gly Ile Thr Val Glu
130 135 140
Gly
145

<210> 311
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (67)..(465)

<223> FRXA02826

<400> 311

ccggacgggtt tctagtgggg tttcatcgctc ccagttgtgg ccggttaacaa ggaagcaggt 60

ttaacg atg gct cct aag aag aag aag aag gtc act ggc ctc atc aag 108
 Met Ala Pro Lys Lys Lys Lys Lys Val Thr Gly Leu Ile Lys
 1 5 10

ctc cag atc cag gca gga cag gca aac cct gct cct cca gtt ggc cca 156
 Leu Gln Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro
 15 20 25 30

gaa ctt ggt gct cac ggc gtc aac atc atg gaa ttc tgc aag gct tac 204
 Glu Leu Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr
 35 40 45

aac gct gcg act gaa aac cag cgc ggg aac gtt gtt cct gtt gag atc 252
 Asn Ala Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile
 50 55 60

acc gtt tac gaa gac cgt tca ttc gac ttc aag ctg aag act cct cca 300
 Thr Val Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro
 65 70 75

gct gca aag ctt ctt ctg aaa gct gct ggc ctg cag aag ggc tcc ggc 348
 Ala Ala Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly
 80 85 90

gtt cct cac acc cag aag gtc ggc aag gtt tcc atg gct cag gtt cgt 396
 Val Pro His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg
 95 100 105 110

gag atc cct gcg acc aag aac gaa gac ctg acg ctc gcg ata tcg acg 444
 Glu Ile Pro Ala Thr Lys Asn Glu Asp Leu Thr Leu Ala Ile Ser Thr
 115 120 125

ctg ctg cga aga tca tcg ctg 465
 Leu Leu Arg Arg Ser Ser Leu
 130

<210> 312

<211> 133

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

Met Ala Pro Lys Lys Lys Lys Lys Val Thr Gly Leu Ile Lys Leu Gln
 1 5 10 15

Ile Gln Ala Gly Gln Ala Asn Pro Ala Pro Pro Val Gly Pro Glu Leu
 20 25 30

Gly Ala His Gly Val Asn Ile Met Glu Phe Cys Lys Ala Tyr Asn Ala
 35 40 45

Ala Thr Glu Asn Gln Arg Gly Asn Val Val Pro Val Glu Ile Thr Val
 50 55 60

Tyr Glu Asp Arg Ser Phe Asp Phe Lys Leu Lys Thr Pro Pro Ala Ala
 65 70 75 80
 Lys Leu Leu Leu Lys Ala Ala Gly Leu Gln Lys Gly Ser Gly Val Pro
 85 90 95
 His Thr Gln Lys Val Gly Lys Val Ser Met Ala Gln Val Arg Glu Ile
 100 105 110
 Pro Ala Thr Lys Asn Glu Asp Leu Thr Leu Ala Ile Ser Thr Leu Leu
 115 120 125
 Arg Arg Ser Ser Leu
 130

<210> 313

<211> 507

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(484)

<223> RXA01334

<400> 313

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 tcgagcgtgt taaacgctca acaacaggaa ggatgccacc atg gct aag ctc acc 115
 Met Ala Lys Leu Thr
 1 5
 aaa gac gag ctc atc gag gct ttc aag gaa atg acc ctc atc gag ctc 163
 Lys Asp Glu Leu Ile Glu Ala Phe Lys Glu Met Thr Leu Ile Glu Leu
 10 15 20
 tcc gag ttc gtt aag gaa ttc gaa gag gtc ttc gac gta acc gca gct 211
 Ser Glu Phe Val Lys Glu Phe Glu Glu Val Phe Asp Val Thr Ala Ala
 25 30 35
 gct cca gtt gca gtt gct gct gca ggc gct gca ggc ggc gaa gct gct 259
 Ala Pro Val Ala Val Ala Ala Ala Gly Ala Ala Gly Gly Glu Ala Ala
 40 45 50
 gct gca gaa gag aag gac gag ttc gac gtc gtt ctc gaa gac gca ggc 307
 Ala Ala Glu Glu Lys Asp Glu Phe Asp Val Val Leu Glu Asp Ala Gly
 55 60 65
 gca aag aag atc ggc gtc atc aag gct gtc cgc gag ctc gtc tcc ggc 355
 Ala Lys Lys Ile Gly Val Ile Lys Ala Val Arg Glu Leu Val Ser Gly
 70 75 80 85
 ctg ggc ctg aag gaa gca aag gag ctc gtt gag ggc gca cct aag gct 403
 Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu Gly Ala Pro Lys Ala
 90 95 100
 atc ctc gag ggc gca aac aag gac gac gct gag gct gca aag gct aag 451
 Ile Leu Glu Gly Ala Asn Lys Asp Asp Ala Glu Ala Ala Lys Ala Lys
 105 110 115

ctc gaa gag gct ggc gca aag gtc acc ctt aag taagaacttt cttacacctt 504
Leu Glu Glu Ala Gly Ala Lys Val Thr Leu Lys
120 125

ttc

507

<210> 314

<211> 128

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

Met Ala Lys Leu Thr Lys Asp Glu Leu Ile Glu Ala Phe Lys Glu Met
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Thr Leu Ile Glu Leu Ser Glu Phe Val Lys Glu Phe Glu Glu Val Phe
20 25 30

Asp Val Thr Ala Ala Ala Pro Val Ala Val Ala Ala Gly Ala Ala
35 40 45

Gly Gly Glu Ala Ala Ala Ala Glu Glu Lys Asp Glu Phe Asp Val Val
50 55 60

Leu Glu Asp Ala Gly Ala Lys Lys Ile Gly Val Ile Lys Ala Val Arg
65 70 75 80

Glu Leu Val Ser Gly Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu
85 90 95

Gly Ala Pro Lys Ala Ile Leu Glu Gly Ala Asn Lys Asp Asp Ala Glu
100 105 110

Ala Ala Lys Ala Lys Leu Glu Glu Ala Gly Ala Lys Val Thr Leu Lys
115 120 125

<210> 315

<211> 353

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(330)

<223> RXA02037

<400> 315

ggc aag ggc aag cct ttg tac gca cct aac gtt gac tgc ggc gac cac 48
Gly Lys Gly Lys Pro Leu Tyr Ala Pro Asn Val Asp Cys Gly Asp His
1 5 10 15

gta atc gtg atc aac gct gac aag gtt gca gtt acc tcc aac aag cgc 96
Val Ile Val Ile Asn Ala Asp Lys Val Ala Val Thr Ser Asn Lys Arg
20 25 30

gag cgc gaa atg cgt tac cgc cac tcc ggt tac cct ggt ggc ctg aag 144

ccacaccgtg atccgccccg ataccccaga ggtacgtggc atgacctgg cagttcgcca 60
cctgatcgtc gtcgaagaag tggcggggga gtaggtaaca atg agc gaa cca att 115
Met Ser Glu Pro Ile
1 5
aag ctc cac gat ttg cgc cca gca gcg ggc tca aac aaa gct aag acc 163
Lys Leu His Asp Leu Arg Pro Ala Ala Gly Ser Asn Lys Ala Lys Thr
10 15 20
cgc gtt ggt cga ggc gaa gca tcc aag ggt aag act gca ggt cgc ggt 211
Arg Val Gly Arg Gly Glu Ala Ser Lys Gly Lys Thr Ala Gly Arg Gly
25 30 35
acc aag ggt acc aag gca cgc aag cag gtt tct gca gca ttc gaa ggt 259
Thr Lys Gly Thr Lys Ala Arg Lys Gln Val Ser Ala Ala Phe Glu Gly
40 45 50
ggc cag atg cca ctg cag atg cgt ctt cct aag ctg aag ggc ttc aag 307
Gly Gln Met Pro Leu Gln Met Arg Leu Pro Lys Leu Lys Gly Phe Lys
55 60 65
aac cct aac aag gtt gac tac cag gta gtt aac att gca gat ctc gca 355
Asn Pro Asn Lys Val Asp Tyr Gln Val Val Asn Ile Ala Asp Leu Ala
70 75 80 85
gag aag ttc cca cag ggc ggc gac gtc agc att gct gac atc gtt gca 403
Glu Lys Phe Pro Gln Gly Gly Asp Val Ser Ile Ala Asp Ile Val Ala
90 95 100
gca gga ctt gtc cgc aag aac gaa ctg gtt aag gtt ctt ggc aac ggc 451
Ala Gly Leu Val Arg Lys Asn Glu Leu Val Lys Val Leu Gly Asn Gly
105 110 115
gac atc agc gtc aag ctg aac gtc acc gct aac aag ttc tcc ggc tct 499
Asp Ile Ser Val Lys Leu Asn Val Thr Ala Asn Lys Phe Ser Gly Ser
120 125 130
gcc aag gaa aag atc gaa gcc gct ggc ggc tcc gca acc gtg gca 544
Ala Lys Glu Lys Ile Glu Ala Ala Gly Gly Ser Ala Thr Val Ala
135 140 145
taagttcacc agaactttaaa aaa 567

<210> 318

<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Met Ser Glu Pro Ile Lys Leu His Asp Leu Arg Pro Ala Ala Gly Ser
1 5 10 15

Asn Lys Ala Lys Thr Arg Val Gly Arg Gly Glu Ala Ser Lys Gly Lys
20 25 30

Thr Ala Gly Arg Gly Thr Lys Gly Thr Lys Ala Arg Lys Gln Val Ser
35 40 45

Ala Ala Phe Glu Gly Gly Gln Met Pro Leu Gln Met Arg Leu Pro Lys

50	55	60
Leu Lys Gly Phe Lys Asn Pro Asn Lys Val Asp Tyr Gln Val Val Asn		
65	70	75 80
Ile Ala Asp Leu Ala Glu Lys Phe Pro Gln Gly Gly Asp Val Ser Ile		
	85	90 95
Ala Asp Ile Val Ala Ala Gly Leu Val Arg Lys Asn Glu Leu Val Lys		
	100	105 110
Val Leu Gly Asn Gly Asp Ile Ser Val Lys Leu Asn Val Thr Ala Asn		
	115	120 125
Lys Phe Ser Gly Ser Ala Lys Glu Lys Ile Glu Ala Ala Gly Gly Ser		
	130	135 140
Ala Thr Val Ala		
145		

<210> 319
 <211> 537
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(514)
 <223> RXA02042

<400> 319
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 agcgtcgtca gcgtgctgag cagaagcagg agggctaaac atg ctt att cct aag 115
 Met Leu Ile Pro Lys 5
 1
 cgc gtt aag tac cgt cgc cag cac cgt cct acc cgt agt ggt atc tcc 163
 Arg Val Lys Tyr Arg Arg Gln His Arg Pro Thr Arg Ser Gly Ile Ser 20
 10 15
 aag ggc ggc aac cgc gtc act ttc ggt gag tac ggc atc cag gct ctc 211
 Lys Gly Gly Asn Arg Val Thr Phe Gly Glu Tyr Gly Ile Gln Ala Leu 35
 25 30
 gag cct gcc tac atc acc aac cgt cag att gaa tct gca cgt att gca 259
 Glu Pro Ala Tyr Ile Thr Asn Arg Gln Ile Glu Ser Ala Arg Ile Ala 50
 40 45
 atc aac cgc cac gtc agg cgt ggt ggc aag gtt tgg atc aac atc ttc 307
 Ile Asn Arg His Val Arg Arg Gly Gly Lys Val Trp Ile Asn Ile Phe 65
 55 60
 cca gac cgc cca ctg acc cag aag cca ctc ggc gtt cgt atg ggt tcc 355
 Pro Asp Arg Pro Leu Thr Gln Lys Pro Leu Gly Val Arg Met Gly Ser 85
 70 75 80
 ggt aag ggc cct gtg gag aag tgg gtt gca aac atc aag ccg ggc cgt 403
 Gly Lys Gly Pro Val Glu Lys Trp Val Ala Asn Ile Lys Pro Gly Arg 100
 90 95 100

atc ctc ttc gag atg agc tac ccg gac gaa gct act gct ctc gag gct 451
Ile Leu Phe Glu Met Ser Tyr Pro Asp Glu Ala Thr Ala Leu Glu Ala
105 110 115

ctg cgc cgc gct ggc cag aag ctt cca tgc aag gtc cgt atc gtc aag 499
Leu Arg Arg Ala Gly Gln Lys Leu Pro Cys Lys Val Arg Ile Val Lys
120 125 130

agg gag gat cag ctc taatggctat cggtacccca gca 537
Arg Glu Asp Gln Leu
135

<210> 320

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

Met Leu Ile Pro Lys Arg Val Lys Tyr Arg Arg Gln His Arg Pro Thr
1 5 10 15

Arg Ser Gly Ile Ser Lys Gly Gly Asn Arg Val Thr Phe Gly Glu Tyr
20 25 30

Gly Ile Gln Ala Leu Glu Pro Ala Tyr Ile Thr Asn Arg Gln Ile Glu
35 40 45

Ser Ala Arg Ile Ala Ile Asn Arg His Val Arg Arg Gly Gly Lys Val
50 55 60

Trp Ile Asn Ile Phe Pro Asp Arg Pro Leu Thr Gln Lys Pro Leu Gly
65 70 75 80

Val Arg Met Gly Ser Gly Lys Gly Pro Val Glu Lys Trp Val Ala Asn
85 90 95

Ile Lys Pro Gly Arg Ile Leu Phe Glu Met Ser Tyr Pro Asp Glu Ala
100 105 110

Thr Ala Leu Glu Ala Leu Arg Arg Ala Gly Gln Lys Leu Pro Cys Lys
115 120 125

Val Arg Ile Val Lys Arg Glu Asp Gln Leu
130 135

<210> 321

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(589)

<223> RXA00670

<400> 321

gaaactggtg gctacatcga tgtcgaggcg gaagattccg agtaagtcgc atggtccaat 60

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<210> 322
<211> 163
<212> PRT
<213> Corynebacterium glutamicum
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<400> 322
Met  Pro  Thr  Pro  Lys  Lys  Gly  Ala  Arg  Leu  Gly  Gly  Ser  Ala  Ser  His
   1              5              10              15

Gln  Lys  Lys  Ile  Leu  Ser  Asn  Leu  Ala  Ala  Ser  Leu  Phe  Glu  His  Gly
          20              25              30

Ala  Ile  Lys  Thr  Thr  Asp  Ala  Lys  Ala  Lys  Ala  Leu  Arg  Pro  Tyr  Ala
      35              40              45

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Glu Lys Leu Ile Thr Lys Ala Lys Ser Gly Ser Val Ala Asp Arg Arg
50 55 60

Asn Val Leu Ala Leu Val Pro Asn Lys Glu Ile Val Ala Tyr Leu Phe
65 70 75 80

Asn Glu Leu Ala Pro Lys Phe Glu Asn Arg Pro Gly Gly Tyr Thr Arg
85 90 95

Ile Ile Lys Leu Glu Asn Arg Lys Gly Asp Asn Ala Pro Met Ser Gln
100 105 110

Ile Ser Leu Val Leu Glu Glu Thr Val Ser Ala Glu Ala Ser Arg Ala
115 120 125

Thr Arg Ala Ser Ala Ser Lys Lys Ala Ala Glu Glu Ala Glu Thr Glu
130 135 140

Glu Val Val Glu Ala Pro Ala Glu Glu Thr Ala Thr Glu Glu Ala Ala
145 150 155 160

Glu Glu Lys

<210> 323

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(502)

<223> RXA00696

<400> 323

gatccgccgc ctgcgtaagg acgatcctta caagggttaag ggcacccgct acgaggggtga 60

gcagatccgc cgcaagggtcg gaaagacggg taagtaagca atg agc aac act gaa 115
Met Ser Asn Thr Glu
1 5

aac aag cag aag cgc gtt tcc gtt ggc aag gac atc gcg act cgt cgt 163
Asn Lys Gln Lys Arg Val Ser Val Gly Lys Asp Ile Ala Thr Arg Arg
10 15 20

cgc gtt gcc cgt gca cgc cgc cac ttc cgc atc cgc aag aac ctg cgt 211
Arg Val Ala Arg Ala Arg Arg His Phe Arg Ile Arg Lys Asn Leu Arg
25 30 35

ggc acc cca gag gct cca cgt ttg gtt gtc cac cgc tct tct cgc cac 259
Gly Thr Pro Glu Ala Pro Arg Leu Val Val His Arg Ser Ser Arg His
40 45 50

atg cac gtt cag atc atc gat gac gtt gca ggc cac acc ctg gct gca 307
Met His Val Gln Ile Ile Asp Asp Val Ala Gly His Thr Leu Ala Ala
55 60 65

gct tct tcc atc gag gct gag gtt cgc gca act gag ggc gac aag aag 355
Ala Ser Ser Ile Glu Ala Glu Val Arg Ala Thr Glu Gly Asp Lys Lys

70 75 80 85

gct aag ggc gca aag gtc ggt cag ctg atc gcc gag cgc gct aag gct 403
Ala Lys Gly Ala Lys Val Gly Gln Leu Ile Ala Glu Arg Ala Lys Ala
 90 95 100

gct ggt atc gag cag gtc gtc ttc gac cgc gct ggt tac aag tac cac 451
Ala Gly Ile Glu Gln Val Val Phe Asp Arg Ala Gly Tyr Lys Tyr His
 105 110 115

ggc cgc gtt gca gct ctc gct gac gcc gct cgt gaa ggt ggt ctg aaa 499
Gly Arg Val Ala Ala Leu Ala Asp Ala Ala Arg Glu Gly Gly Leu Lys
 120 125 130

ttc taatgatgac catttctaag aac 525
Phe

<210> 324
<211> 134
<212> PRT
<213> Corynebacterium glutamicum

<400> 324
Met Ser Asn Thr Glu Asn Lys Gln Lys Arg Val Ser Val Gly Lys Asp
1 5 10 15

Ile Ala Thr Arg Arg Arg Val Ala Arg Ala Arg Arg His Phe Arg Ile
 20 25 30

Arg Lys Asn Leu Arg Gly Thr Pro Glu Ala Pro Arg Leu Val Val His
 35 40 45

Arg Ser Ser Arg His Met His Val Gln Ile Ile Asp Asp Val Ala Gly
50 55 60

His Thr Leu Ala Ala Ala Ser Ser Ile Glu Ala Glu Val Arg Ala Thr
65 70 75 80

Glu Gly Asp Lys Lys Ala Lys Gly Ala Lys Val Gly Gln Leu Ile Ala
 85 90 95

Glu Arg Ala Lys Ala Ala Gly Ile Glu Gln Val Val Phe Asp Arg Ala
100 105 110

Gly Tyr Lys Tyr His Gly Arg Val Ala Ala Leu Ala Asp Ala Ala Arg
115 120 125

Glu Gly Gly Leu Lys Phe
130

<210> 325
<211> 462
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(439)

<223> RXA01353

<400> 325

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gccagggtcc tctttcccta ctagtaaaag gattgtttat atg aac att ctg gat 115
Met Asn Ile Leu Asp
1 5

aag atc gac gca gca tcc ctg cgc gac gac gtt cct gca ttc cgc gcc 163
Lys Ile Asp Ala Ala Ser Leu Arg Asp Asp Val Pro Ala Phe Arg Ala
10 15 20

ggc gac acc ctc gac gta cac gtc aag gtc atc gaa ggc acc acc acc 211
Gly Asp Thr Leu Asp Val His Val Lys Val Ile Glu Gly Thr Thr Thr
25 30 35

cgt acc cag ctg ttc aag ggt gtt gtc att cgc cgt cag ggc ggc gga 259
Arg Thr Gln Leu Phe Lys Gly Val Val Ile Arg Arg Gln Gly Gly Gly
40 45 50

atc cgc gag acc ttc acc gta cgt aag gtt tcc ttc ggc atc ggt gtt 307
Ile Arg Glu Thr Phe Thr Val Arg Lys Val Ser Phe Gly Ile Gly Val
55 60 65

gag cgt acc ttc cca gta cac tcc cca aac atc gag aag atc gag gtc 355
Glu Arg Thr Phe Pro Val His Ser Pro Asn Ile Glu Lys Ile Glu Val
70 75 80 85

att cgt cgt ggt gac gtt cgt cgt gcg aag ctg tac tac ctg cgc gaa 403
Ile Arg Arg Gly Asp Val Arg Arg Ala Lys Leu Tyr Tyr Leu Arg Glu
90 95 100

ctg cgc ggc aag gct gca cgt att aag gag aag cgc taattattta 449
Leu Arg Gly Lys Ala Ala Arg Ile Lys Glu Lys Arg
105 110

gcgtttgtta ggt 462

<210> 326

<211> 113

<212> PRT

<213> Corynebacterium glutamicum

<400> 326

Met Asn Ile Leu Asp Lys Ile Asp Ala Ala Ser Leu Arg Asp Asp Val
1 5 10 15

Pro Ala Phe Arg Ala Gly Asp Thr Leu Asp Val His Val Lys Val Ile
20 25 30

Glu Gly Thr Thr Thr Arg Thr Gln Leu Phe Lys Gly Val Val Ile Arg
35 40 45

Arg Gln Gly Gly Gly Ile Arg Glu Thr Phe Thr Val Arg Lys Val Ser
50 55 60

Phe Gly Ile Gly Val Glu Arg Thr Phe Pro Val His Ser Pro Asn Ile
65 70 75 80

<400> 327																
cgacaccaag cgcatgaagc gcctgctcgg caaggcttaa gtttaaaacc ttcgcctaaa																60
cccctccacc tttcaagaca agattttaagg aagtaccacc																115
Val Ala Arg Val Lys																5
1																
cgg tcc gtt aac gca aag aag aag cgt cgc gaa att ctg aag tcc gca																163
Arg Ser Val Asn Ala Lys Lys Lys Arg Arg Glu Ile Leu Lys Ser Ala																20
10 15																
aag ggc tac cgc ggc cag cgc tca cgc ctt tac cgt aag gct aag gag																211
Lys Gly Tyr Arg Gly Gln Arg Ser Arg Leu Tyr Arg Lys Ala Lys Glu																35
25 30																
cag tgg ctg cac tcc atg act tac tct tac cgc gat cgt cgc gcc cgt																259
Gln Trp Leu His Ser Met Thr Tyr Ser Tyr Arg Asp Arg Arg Ala Arg																50
40 45																
aag agc gag ttc cgt aag ctg tgg atc cag cgt atc aac gct gct gca																307
Lys Ser Glu Phe Arg Lys Leu Trp Ile Gln Arg Ile Asn Ala Ala Ala																65
55 60																
cgt atg aac ggc atc acc tac aac cgt ctc atc cag ggc ctt cgc ctt																355
Arg Met Asn Gly Ile Thr Tyr Asn Arg Leu Ile Gln Gly Leu Arg Leu																85
70 75 80																
gct gag atc gag gtc gac cgc aag atc ctc gct gat ctc gca gtc aac																403
Ala Glu Ile Glu Val Asp Arg Lys Ile Leu Ala Asp Leu Ala Val Asn																100
90 95 100																
gac ttt gca acc ttc tcc gca atc tgc gag gct gca aag gct gca ctt																451
Asp Phe Ala Thr Phe Ser Ala Ile Cys Glu Ala Ala Lys Ala Ala Leu																115
105 110																
cct gag gac gtt aac gct cca aag gct gct taagcttaca aacgaattga																501
Pro Glu Asp Val Asn Ala Pro Lys Ala Ala																125
120																
cct																504

<210> 328
<211> 127
<212> PRT
<213> Corynebacterium glutamicum

<400> 328
Val Ala Arg Val Lys Arg Ser Val Asn Ala Lys Lys Lys Arg Arg Glu
1 5 10 15
Ile Leu Lys Ser Ala Lys Gly Tyr Arg Gly Gln Arg Ser Arg Leu Tyr
20 25 30
Arg Lys Ala Lys Glu Gln Trp Leu His Ser Met Thr Tyr Ser Tyr Arg
35 40 45
Asp Arg Arg Ala Arg Lys Ser Glu Phe Arg Lys Leu Trp Ile Gln Arg
50 55 60
Ile Asn Ala Ala Ala Arg Met Asn Gly Ile Thr Tyr Asn Arg Leu Ile
65 70 75 80
Gln Gly Leu Arg Leu Ala Glu Ile Glu Val Asp Arg Lys Ile Leu Ala
85 90 95
Asp Leu Ala Val Asn Asp Phe Ala Thr Phe Ser Ala Ile Cys Glu Ala
100 105 110
Ala Lys Ala Ala Leu Pro Glu Asp Val Asn Ala Pro Lys Ala Ala
115 120 125

<210> 329
<211> 415
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(415)
<223> RXN02371

<400> 329
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cgagtacctg agccgagaat cagataaggg gtagccctct atg tac gcg atc gtc 115
Met Tyr Ala Ile Val
1 5
aag acc ggc gga aag cag tac aag gtt gcc gaa ggt gac ctc gtt aag 163
Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu Gly Asp Leu Val Lys
10 15 20
gtc gag aag atc gag ggt gag ccg ggt gca tcc gtg gct ctc acc ccg 211
Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser Val Ala Leu Thr Pro
25 30 35
gtt ctg ctc gtc gat ggc gcc gat gta acc acc gcc gct gac aag ctc 259
Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr Ala Ala Asp Lys Leu
40 45 50

gct tct gtg agc gtc aac acc gag atc gtc gag cac acc aag ggc ccg 307
Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu His Thr Lys Gly Pro
55 60 65

aag atc aag atc ctg aag tac aag aac aag acc gga tac aag aag cgc 355
Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr Gly Tyr Lys Lys Arg
70 75 80 85

cag gga cac cgt cag ccc ctg acc gtt ctg aag gta acc gga aat caa 403
Gln Gly His Arg Gln Pro Leu Thr Val Leu Lys Val Thr Gly Asn Gln
90 95 100

gta agc cct cgg 415
Val Ser Pro Arg
105

<210> 330

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 330

Met Tyr Ala Ile Val Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu
1 5 10 15

Gly Asp Leu Val Lys Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser
20 25 30

Val Ala Leu Thr Pro Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr
35 40 45

Ala Ala Asp Lys Leu Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu
50 55 60

His Thr Lys Gly Pro Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr
65 70 75 80

Gly Tyr Lys Lys Arg Gln Gly His Arg Gln Pro Leu Thr Val Leu Lys
85 90 95

Val Thr Gly Asn Gln Val Ser Pro Arg
100 105

<210> 331

<211> 370

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(370)

<223> FRXA02371

<400> 331

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cgagtacctg agccgagaat cagataaggg gtagccctct atg tac gcg atc gtc 115
Met Tyr Ala Ile Val
1 5

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aag acc ggc gga aag cag tac aag gtt gcc gaa ggt gac ctc gtt aag 163
Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu Gly Asp Leu Val Lys
      10                      15                      20

gtc gag aag atc gag ggt gag ccg ggt gca tcc gtg gct ctc acc ccg 211
Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser Val Ala Leu Thr Pro
      25                      30                      35

gtt ctg ctc gtc gat ggc gcc gat gta acc acc gcc gct gac aag ctc 259
Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr Ala Ala Asp Lys Leu
      40                      45                      50

gct tct gtg agc gtc aac acc gag atc gtc gag cac acc aag ggc ccg 307
Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu His Thr Lys Gly Pro
      55                      60                      65

aag atc aag atc ctg aag tac aag aac aag acc gga tac aag aag cgc 355
Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr Gly Tyr Lys Lys Arg
      70                      75                      80                      85

cag gga cac cgt cag
Gln Gly His Arg Gln
      90

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<210> 332
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

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<400> 332
Met Tyr Ala Ile Val Lys Thr Gly Gly Lys Gln Tyr Lys Val Ala Glu
  1              5              10              15

Gly Asp Leu Val Lys Val Glu Lys Ile Glu Gly Glu Pro Gly Ala Ser
      20              25              30

Val Ala Leu Thr Pro Val Leu Leu Val Asp Gly Ala Asp Val Thr Thr
      35              40              45

Ala Ala Asp Lys Leu Ala Ser Val Ser Val Asn Thr Glu Ile Val Glu
      50              55              60

His Thr Lys Gly Pro Lys Ile Lys Ile Leu Lys Tyr Lys Asn Lys Thr
      65              70              75              80

Gly Tyr Lys Lys Arg Gln Gly His Arg Gln
      85              90

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<210> 333
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(403)
<223> RXA01949

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<400> 333

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tcaaccgcgc ttccggtgcg gcacaggagg agcagaacta atg gct act atc gcc 115
 Met Ala Thr Ile Ala
 1 5

aac cca cgc gac atc atc atc gca ccg gtc gtt tct gag aag tcc tac 163
 Asn Pro Arg Asp Ile Ile Ile Ala Pro Val Val Ser Glu Lys Ser Tyr
 10 15 20

ggc ctc atg gag cag aac gtt tac acg ttc ttc gtc tcc act gac gct 211
 Gly Leu Met Glu Gln Asn Val Tyr Thr Phe Phe Val Ser Thr Asp Ala
 25 30 35

aac aag act cag atc aag att gcc atc gaa gag atc ttc ggc gtc aag 259
 Asn Lys Thr Gln Ile Lys Ile Ala Ile Glu Glu Ile Phe Gly Val Lys
 40 45 50

gtt gca tct gtg aac acc gtt aac cgt gca ggt aag cgc aag cgc tcc 307
 Val Ala Ser Val Asn Thr Val Asn Arg Ala Gly Lys Arg Lys Arg Ser
 55 60 65

cgc acc ggc ttc ggt act cgc aag gct acc aag cgc gct tat gtg act 355
 Arg Thr Gly Phe Gly Thr Arg Lys Ala Thr Lys Arg Ala Tyr Val Thr
 70 75 80 85

ctt cgc gaa ggc agc gac tcc atc gac atc ttc agc ggc tcc gtc gct 403
 Leu Arg Glu Gly Ser Asp Ser Ile Asp Ile Phe Ser Gly Ser Val Ala
 90 95 100

taagacgtcg atagaaaagg aca 426

<210> 334

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

Met Ala Thr Ile Ala Asn Pro Arg Asp Ile Ile Ile Ala Pro Val Val
 1 5 10 15

Ser Glu Lys Ser Tyr Gly Leu Met Glu Gln Asn Val Tyr Thr Phe Phe
 20 25 30

Val Ser Thr Asp Ala Asn Lys Thr Gln Ile Lys Ile Ala Ile Glu Glu
 35 40 45

Ile Phe Gly Val Lys Val Ala Ser Val Asn Thr Val Asn Arg Ala Gly
 50 55 60

Lys Arg Lys Arg Ser Arg Thr Gly Phe Gly Thr Arg Lys Ala Thr Lys
 65 70 75 80

Arg Ala Tyr Val Thr Leu Arg Glu Gly Ser Asp Ser Ile Asp Ile Phe
 85 90 95

Ser Gly Ser Val Ala
 100

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<220>
<221> CDS
<222> (101)..(466)
<223> RXN00709
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<400> 335																	
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ggaaatccag				cacgcattaa	tccagggtcag	gagaccagta		gtg	att	cag	cag	gaa		115			
								Val	Ile	Gln	Gln	Glu		5			
								1									
tcg	cgt	ctg	aag	gtc	gcc	gac	aac	act	ggt	gca	cgt	gaa	att	ctg	tcg	163	
Ser	Arg	Leu	Lys	Val	Ala	Asp	Asn	Thr	Gly	Ala	Arg	Glu	Ile	Leu	Cys		
				10					15								
														20			
atc	cgc	gtt	ctc	ggc	gga	tcc	acc	cga	cgt	ttt	gct	ggc	att	ggc	gac	211	
Ile	Arg	Val	Leu	Gly	Gly	Ser	Thr	Arg	Arg	Phe	Ala	Gly	Ile	Gly	Asp		
				25					30								
													35				
gtc	atc	gtc	gcc	act	gtc	aag	gaa	gca	acc	cca	ggc	ggc	aac	gta	aag	259	
Val	Ile	Val	Ala	Thr	Val	Lys	Glu	Ala	Thr	Pro	Gly	Gly	Asn	Val	Lys		
				40					45								
												50					
tct	ggc	gaa	atc	gtc	aag	gct	gtt	atc	gtt	cgc	acc	aag	aag	gag	acc	307	
Ser	Gly	Glu	Ile	Val	Lys	Ala	Val	Ile	Val	Arg	Thr	Lys	Lys	Glu	Thr		
				55					60								
												65					
cgt	cgt	gca	gac	ggc	tct	tac	atc	tcc	ttc	gat	gag	aac	gct	gcc	gtc	355	
Arg	Arg	Ala	Asp	Gly	Ser	Tyr	Ile	Ser	Phe	Asp	Glu	Asn	Ala	Ala	Val		
				70					75								
												80				85	
atc	atc	aag	aac	gac	aac	gag	cca	cgt	ggc	acc	cgt	atc	ttc	gga	cca	403	
Ile	Ile	Lys	Asn	Asp	Asn	Glu	Pro	Arg	Gly	Thr	Arg	Ile	Phe	Gly	Pro		
				90					95								
														100			
gtt	gct	cgt	gaa	ctt	cgt	gag	aag	aag	ttc	atg	aag	atc	gtt	tct	ctc	451	
Val	Ala	Arg	Glu	Leu	Arg	Glu	Lys	Lys	Phe	Met	Lys	Ile	Val	Ser	Leu		
				105					110								
														115			
gca	ccg	gag	gtg	att	taagaatgaa		gggccacaag		ggc							489	
Ala	Pro	Glu	Val	Ile													
				120													

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<210> 336
<211> 122
<212> PRT
<213> Corynebacterium glutamicum
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Arg Glu Ile Leu Cys Ile Arg Val Leu Gly Gly Ser Thr Arg Arg Phe

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Ala Gly Ile Gly Asp Val Ile Val Ala Thr Val Lys Glu Ala Thr Pro		
35	40	45
Gly Gly Asn Val Lys Ser Gly Glu Ile Val Lys Ala Val Ile Val Arg		
50	55	60
Thr Lys Lys Glu Thr Arg Arg Ala Asp Gly Ser Tyr Ile Ser Phe Asp		
65	70	75
Glu Asn Ala Ala Val Ile Ile Lys Asn Asp Asn Glu Pro Arg Gly Thr		
85	90	95
Arg Ile Phe Gly Pro Val Ala Arg Glu Leu Arg Glu Lys Lys Phe Met		
100	105	110
Lys Ile Val Ser Leu Ala Pro Glu Val Ile		
115	120	

<210> 337

<211> 362

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(339)

<223> FRXA00709

<400> 337

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ggt gga tcc acc cga cgt ttt gct ggc att ggt gac gtc atc gtc gcc	96
Gly Gly Ser Thr Arg Arg Phe Ala Gly Ile Gly Asp Val Ile Val Ala	
20 25 30	
act gtc aag gaa gca acc cca ggc ggc aac gta aag tct ggc gaa atc	144
Thr Val Lys Glu Ala Thr Pro Gly Gly Asn Val Lys Ser Gly Glu Ile	
35 40 45	
gtc aag gct gtt atc gtt cgc acc aag aag gag acc cgt cgt gca gac	192
Val Lys Ala Val Ile Val Arg Thr Lys Lys Glu Thr Arg Arg Ala Asp	
50 55 60	
ggt tct tac atc tcc ttc gat gag aac gct gcc gtc atc atc aag aac	240
Gly Ser Tyr Ile Ser Phe Asp Glu Asn Ala Ala Val Ile Ile Lys Asn	
65 70 75 80	
gac aac gag cca cgt ggc acc cgt atc ttc gga cca gtt gct cgt gaa	288
Asp Asn Glu Pro Arg Gly Thr Arg Ile Phe Gly Pro Val Ala Arg Glu	
85 90 95	
ctt cgt gag aag aag ttc atg aag atc gtt tct ctc gca ccg gag gtg	336
Leu Arg Glu Lys Lys Phe Met Lys Ile Val Ser Leu Ala Pro Glu Val	
100 105 110	
att taagaatgaa ggtccacaag ggc	362


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<400> 339
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tcatgaagat cgtttctctc gcaccggagg tgatttaaga atg aag gtc cac aag 115
                                         Met Lys Val His Lys
                                         1                               5

ggc gat atg gtt ctg gtc atc tca ggt cca gac aag ggt gct aag gga 163
Gly Asp Met Val Leu Val Ile Ser Gly Pro Asp Lys Gly Ala Lys Gly
                        10                               15                               20

cag gtc atc gcg gct ttc cct aag acc gaa aag gtt ctc gtc gaa ggc 211
Gln Val Ile Ala Ala Phe Pro Lys Thr Glu Lys Val Leu Val Glu Gly
                        25                               30                               35

gtt aac cgc atc aag aag cac gta qct aac tcc qca cca qag cgt ggc 259

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Val Asn Arg Ile Lys Lys His Val Ala Asn Ser Ala Pro Glu Arg Gly
 40 45 50
 gca gag tcc ggc gga atc gtg acc cag gaa gct ccg atc cat gtc tct 307
 Ala Glu Ser Gly Gly Ile Val Thr Gln Glu Ala Pro Ile His Val Ser
 55 60 65
 aac gtc atg gtc atc gac tcc gac gga aac cca act cgc gtt ggc tac 355
 Asn Val Met Val Ile Asp Ser Asp Gly Asn Pro Thr Arg Val Gly Tyr
 70 75 80 85
 cgt ttc gat gaa aac ggc aag aag gtc cgc gtt tct cgt cgc aat ggg 403
 Arg Phe Asp Glu Asn Gly Lys Lys Val Arg Val Ser Arg Arg Asn Gly
 90 95 100
 aag gat atc taatgactga gaattacatc cct 435
 Lys Asp Ile

<210> 340
 <211> 104
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 340
 Met Lys Val His Lys Gly Asp Met Val Leu Val Ile Ser Gly Pro Asp
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 20 25 30
 Val Leu Val Glu Gly Val Asn Arg Ile Lys Lys His Val Ala Asn Ser
 35 40 45
 Ala Pro Glu Arg Gly Ala Glu Ser Gly Gly Ile Val Thr Gln Glu Ala
 50 55 60
 Pro Ile His Val Ser Asn Val Met Val Ile Asp Ser Asp Gly Asn Pro
 65 70 75 80
 Thr Arg Val Gly Tyr Arg Phe Asp Glu Asn Gly Lys Lys Val Arg Val
 85 90 95
 Ser Arg Arg Asn Gly Lys Asp Ile
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<210> 341
 <211> 357
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(334)
 <223> RXA02635

<400> 341
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gtcttctaac tgaatgtggg cggctaggag aaagtaagtt atg tcg gca cat tgc 115
Met Ser Ala His Cys
1 5

cag gta acg gga cgc aag ccg agt ttc ggc aag tct gtc tca cac tcg 163
Gln Val Thr Gly Arg Lys Pro Ser Phe Gly Lys Ser Val Ser His Ser
10 15 20

cac cga cgc act tcc cgc cgt tgg aac ccc aac gtg cag cgt cgc aag 211
His Arg Arg Thr Ser Arg Arg Trp Asn Pro Asn Val Gln Arg Arg Lys
25 30 35

ttc tat gtc cct tcc gag gga cgc acc atc act ctg acc gtt tcc acc 259
Phe Tyr Val Pro Ser Glu Gly Arg Thr Ile Thr Leu Thr Val Ser Thr
40 45 50

aag ggt ctg aag gtc att gac cgc gac ggc atc gaa gcc gtt gtt gct 307
Lys Gly Leu Lys Val Ile Asp Arg Asp Gly Ile Glu Ala Val Val Ala
55 60 65

cag att cgc gca cgt ggg gag aag atc taaagatggc acgtaatgat 354
Gln Ile Arg Ala Arg Gly Glu Lys Ile
70 75

atc 357

<210> 342

<211> 78

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

Met Ser Ala His Cys Gln Val Thr Gly Arg Lys Pro Ser Phe Gly Lys
1 5 10 15

Ser Val Ser His Ser His Arg Arg Thr Ser Arg Arg Trp Asn Pro Asn
20 25 30

Val Gln Arg Arg Lys Phe Tyr Val Pro Ser Glu Gly Arg Thr Ile Thr
35 40 45

Leu Thr Val Ser Thr Lys Gly Leu Lys Val Ile Asp Arg Asp Gly Ile
50 55 60

Glu Ala Val Val Ala Gln Ile Arg Ala Arg Gly Glu Lys Ile
65 70 75

<210> 343

<211> 241

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(241)

<223> RXA02043

<400> 343

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catgcaaggt ccgtatcgtc aagagggagg atcagctcta atg gct atc ggt acc 115
 Met Ala Ile Gly Thr
 1 5

cca gca cac gag ttc cgt gag ctc aac gag gaa gaa ctg gtt acc cgc 163
 Pro Ala His Glu Phe Arg Glu Leu Asn Glu Glu Glu Leu Val Thr Arg
 10 15 20

ctc aac gag gct aag gaa gaa ctg ttc aac ctt cgc ttc cag ctt gcc 211
 Leu Asn Glu Ala Lys Glu Glu Leu Phe Asn Leu Arg Phe Gln Leu Ala
 25 30 35

acc ggc cag ctg acc aac aac cgc cgc ctg 241
 Thr Gly Gln Leu Thr Asn Asn Arg Arg Leu
 40 45

<210> 344

<211> 47

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Met Ala Ile Gly Thr Pro Ala His Glu Phe Arg Glu Leu Asn Glu Glu
 1 5 10 15

Glu Leu Val Thr Arg Leu Asn Glu Ala Lys Glu Glu Leu Phe Asn Leu
 20 25 30

Arg Phe Gln Leu Ala Thr Gly Gln Leu Thr Asn Asn Arg Arg Leu
 35 40 45

<210> 345

<211> 306

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(283)

<223> RXA00698

<400> 345

gggccgccct gaagaggttg cagcccgccg tggcaagacc atcgaagagg tcgcaccagc 60

acgtattctg cgtgcacgcg caggtcagga ggcgtaagaa atg gcg ctg aag att 115
 Met Ala Leu Lys Ile
 1 5

act cag atc aaa ggc act gtg ggc acc aag ccc aag cat cgc gaa aat 163
 Thr Gln Ile Lys Gly Thr Val Gly Thr Lys Pro Lys His Arg Glu Asn
 10 15 20

ctt cgt tcc ctc ggt ctg aag cga atc cgc cac acc gtg atc cgc ccc 211
 Leu Arg Ser Leu Gly Leu Lys Arg Ile Arg His Thr Val Ile Arg Pro
 25 30 35

gat acc cca gag gta cgt ggc atg atc ctg gca gtt cgc cac ctg atc 259
 Asp Thr Pro Glu Val Arg Gly Met Ile Leu Ala Val Arg His Leu Ile

70

75

80

85

aag aag gca taggagggaa aacaatggca gtt
Lys Lys Ala

387

<210> 348

<211> 88

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met Lys Lys Asp Ile His Pro Asp Tyr His Ala Val Val Phe Gln Asp
1 5 10 15

Ala Gly Thr Gly Phe Gln Phe Leu Thr Lys Ser Thr Ala Ser Ser Asp
20 25 30

Arg Thr Val Ser Trp Glu Asp Gly Asn Glu Tyr Pro Leu Ile Val Val
35 40 45

Asp Val Thr Ser Glu Ser His Pro Phe Trp Thr Gly Ala Gln Arg Val
50 55 60

Met Asp Thr Ala Gly Arg Val Glu Lys Phe Glu Arg Arg Phe Gly Gly
65 70 75 80

Met Ala Arg Arg Lys Lys Lys Ala
85

<210> 349

<211> 285

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(262)

<223> RXA02636

<400> 349

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ttgttgctca gattcgcgca cgtggggaga agatctaaag atg gca cgt aat gat 115
Met Ala Arg Asn Asp
1 5

atc cgc cct atc atc aag ctg aag tct act gct ggc act ggt tac acc 163
Ile Arg Pro Ile Ile Lys Leu Lys Ser Thr Ala Gly Thr Gly Tyr Thr
10 15 20

tat gtc acc cgt aag aac aag cgc aac aac ccg gac cgt att tcc ctc 211
Tyr Val Thr Arg Lys Asn Lys Arg Asn Asn Pro Asp Arg Ile Ser Leu
25 30 35

atg aag tac gat cca gta gtc cgt aag cac gtc gaa ttc cgc gag gag 259
Met Lys Tyr Asp Pro Val Val Arg Lys His Val Glu Phe Arg Glu Glu
40 45 50

cga taatcaatgg ctaagaagtc aaa
Arg

285

<210> 350
<211> 54
<212> PRT
<213> Corynebacterium glutamicum

<400> 350
Met Ala Arg Asn Asp Ile Arg Pro Ile Ile Lys Leu Lys Ser Thr Ala
1 5 10 15
Gly Thr Gly Tyr Thr Tyr Val Thr Arg Lys Asn Lys Arg Asn Asn Pro
20 25 30
Asp Arg Ile Ser Leu Met Lys Tyr Asp Pro Val Val Arg Lys His Val
35 40 45
Glu Phe Arg Glu Glu Arg
50

<210> 351
<211> 264
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(241)
<223> RXA01423

<400> 351
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gtccggtgat ccgtcaacaa aatatttagg agtgtttcac atg gca aag ggc aag 115
Met Ala Lys Gly Lys
1 5
cgg acg ttc cag ccg aac aac cgt cgt cgt gca cgt gtt cac ggt ttc 163
Arg Thr Phe Gln Pro Asn Asn Arg Arg Arg Ala Arg Val His Gly Phe
10 15 20
cgt ctt cgt atg cgt acc cgt gca ggt cgt gca att gtt gcg gct cgt 211
Arg Leu Arg Met Arg Thr Arg Ala Gly Arg Ala Ile Val Ala Ala Arg
25 30 35
cgt cgc aag ggt cgc gca aag ctg acc gcg taatttttta gcgtcaccac 261
Arg Arg Lys Gly Arg Ala Lys Leu Thr Ala
40 45
aat 264

<210> 352
<211> 47
<212> PRT
<213> Corynebacterium glutamicum

<400> 352

Met Ala Lys Gly Lys Arg Thr Phe Gln Pro Asn Asn Arg Arg Arg Ala
1 5 10 15

Arg Val His Gly Phe Arg Leu Arg Met Arg Thr Arg Ala Gly Arg Ala
20 25 30

Ile Val Ala Ala Arg Arg Arg Lys Gly Arg Ala Lys Leu Thr Ala
35 40 45

<210> 353

<211> 315

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(292)

<223> RXA02419

<400> 353

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ggcaagaaat aatcacgaat aggggtttaag gacaactttc atg aag aac aag acc 115
Met Lys Asn Lys Thr
1 5

cac aag ggc acc gca aag cgc gtt aag gtg act ggc tcc ggc aag ctc 163
His Lys Gly Thr Ala Lys Arg Val Lys Val Thr Gly Ser Gly Lys Leu
10 15 20

gtt cgc gag cag gca aac cgc cgc cac ctt ctc gag ggc aag tca tct 211
Val Arg Glu Gln Ala Asn Arg Arg His Leu Leu Glu Gly Lys Ser Ser
25 30 35

acc cgc act cgt cgc ctg aag ggc atc gtt gag gtt gac aag gcc gac 259
Thr Arg Thr Arg Arg Leu Lys Gly Ile Val Glu Val Asp Lys Ala Asp
40 45 50

acc aag cgc atg aag cgc ctg ctc ggc aag gct taagtttaaa accttcgcct 312
Thr Lys Arg Met Lys Arg Leu Leu Gly Lys Ala
55 60

aaa 315

<210> 354

<211> 64

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

Met Lys Asn Lys Thr His Lys Gly Thr Ala Lys Arg Val Lys Val Thr
1 5 10 15

Gly Ser Gly Lys Leu Val Arg Glu Gln Ala Asn Arg Arg His Leu Leu
20 25 30

Glu Gly Lys Ser Ser Thr Arg Thr Arg Arg Leu Lys Gly Ile Val Glu
35 40 45

Val Asp Lys Ala Asp Thr Lys Arg Met Lys Arg Leu Leu Gly Lys Ala
 50 55 60

<210> 355
 <211> 1581
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1558)
 <223> RXA02190

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 ccattatcta atttcctatc catttcggag caattttacat atg ccc acc aac aat 115
 Met Pro Thr Asn Asn
 1 5
 gca cct cag gta gcc atc aac gac att ggc tct gct gag gac ttc ctt 163
 Ala Pro Gln Val Ala Ile Asn Asp Ile Gly Ser Ala Glu Asp Phe Leu
 10 15 20
 gca gca atc gac gca acc atc aag tac ttc aac gat ggc gat atc gtt 211
 Ala Ala Ile Asp Ala Thr Ile Lys Tyr Phe Asn Asp Gly Asp Ile Val
 25 30 35
 gaa ggc acc gtg gta aag gtc gat cgt gac gag gta ctt ctc gac atc 259
 Glu Gly Thr Val Val Lys Val Asp Arg Asp Glu Val Leu Leu Asp Ile
 40 45 50
 gga tac aag acc gag ggt gtc atc cca tcc cgc gag ctg tcc atc aag 307
 Gly Tyr Lys Thr Glu Gly Val Ile Pro Ser Arg Glu Leu Ser Ile Lys
 55 60 65
 cac gat gtc gat cca gac gag gtc gtc gaa gtc ggc gac caa att gac 355
 His Asp Val Asp Pro Asp Glu Val Val Glu Val Gly Asp Gln Ile Asp
 70 75 80 85
 gca ctt gtc ctc acc aag gaa gac aaa gaa ggt cgt ctg atc ctt tcc 403
 Ala Leu Val Leu Thr Lys Glu Asp Lys Glu Gly Arg Leu Ile Leu Ser
 90 95 100
 aag aag cgt gct cag tac gag cgt gct tgg ggc gcc atc gag gag ctc 451
 Lys Lys Arg Ala Gln Tyr Glu Arg Ala Trp Gly Ala Ile Glu Glu Leu
 105 110 115
 aag gaa aag gac gag cca gtt acc ggt acc gtc atc gag gtc gtc aag 499
 Lys Glu Lys Asp Glu Pro Val Thr Gly Thr Val Ile Glu Val Val Lys
 120 125 130
 ggt ggc ctc atc atc gac atc ggt ctc cgt ggc ttc ctg cct gca tcc 547
 Gly Gly Leu Ile Ile Asp Ile Gly Leu Arg Gly Phe Leu Pro Ala Ser
 135 140 145

ctc gtt gag atg cgt cgc gtc cgc gac ctg gat ccg tac atc ggc cag Leu Val Glu Met Arg Arg Val Arg Asp Leu Asp Pro Tyr Ile Gly Gln 150 155 160 165	595
gag ctc gaa gct aag atc atc gag ctg gac aag aac cgc aac aac gtc Glu Leu Glu Ala Lys Ile Ile Glu Leu Asp Lys Asn Arg Asn Asn Val 170 175 180	643
gtt ctg tcc cgt cgc gca ttc ctc gag cag acc cag tct gag gtc cgc Val Leu Ser Arg Arg Ala Phe Leu Glu Gln Thr Gln Ser Glu Val Arg 185 190 195	691
tcc gag ttc ctg cac cag ctc cag aag ggc cag gtc cgc aag ggc gtc Ser Glu Phe Leu His Gln Leu Gln Lys Gly Gln Val Arg Lys Gly Val 200 205 210	739
gtc tct tcc atc gtc aac ttc ggc gca ttc gtc gat ctc ggc ggt gtc Val Ser Ser Ile Val Asn Phe Gly Ala Phe Val Asp Leu Gly Gly Val 215 220 225	787
gac gga ctg gtt cac gtt tcc gag ctg tcc tgg aag cac atc gac cac Asp Gly Leu Val His Val Ser Glu Leu Ser Trp Lys His Ile Asp His 230 235 240 245	835
cca tct gag gtt gtc acc gtc ggc gac gaa gtc acc gtt gag gtt ctc Pro Ser Glu Val Val Thr Val Gly Asp Glu Val Thr Val Glu Val Leu 250 255 260	883
gag gtc gat ctc gac cgc gag cgc gtc tcc ctg tcc ctg aag gct acc Glu Val Asp Leu Asp Arg Glu Arg Val Ser Leu Ser Leu Lys Ala Thr 265 270 275	931
cag gaa gac cca tgg cgc gtc ttc gct cgc act cac gct gtg ggc cag Gln Glu Asp Pro Trp Arg Val Phe Ala Arg Thr His Ala Val Gly Gln 280 285 290	979
atc gtt cca ggc aag gtc acc aag ctg gtt cca ttc ggt gcg ttc gtt Ile Val Pro Gly Lys Val Thr Lys Leu Val Pro Phe Gly Ala Phe Val 295 300 305	1027
cgc gtc gaa gag ggc atc gaa ggc ctc gtc cac atc tcc gag ctg gct Arg Val Glu Glu Gly Ile Glu Gly Leu Val His Ile Ser Glu Leu Ala 310 315 320 325	1075
cag cgc cac gtc gag gtt ccg gac cag gtt gtc gca gtt ggc gaa gag Gln Arg His Val Glu Val Pro Asp Gln Val Val Ala Val Gly Glu Glu 330 335 340	1123
gtc atg gtc aag gtc atc gac atc gat ctc gag cgt cgt cgt atc tcc Val Met Val Lys Val Ile Asp Ile Asp Leu Glu Arg Arg Arg Ile Ser 345 350 355	1171
ctg tcc ctc aag cag gct gac gag gac tac acc gaa gag ttc gac cca Leu Ser Leu Lys Gln Ala Asp Glu Asp Tyr Thr Glu Glu Phe Asp Pro 360 365 370	1219
tcc aag tac gga atg gct gac tcc tac gac gag cag ggt aac tac atc Ser Lys Tyr Gly Met Ala Asp Ser Tyr Asp Glu Gln Gly Asn Tyr Ile 375 380 385	1267
ttc cct gag ggc ttc gac gcc gag acc aac gaa tgg ctc gaa ggc ttc	1315

Phe Pro Glu Gly Phe Asp Ala Glu Thr Asn Glu Trp Leu Glu Gly Phe
 390 395 400 405
 gat gag cag cgt cag gct tgg gaa gct cgc tac gcc gag tcc gag cgt 1363
 Asp Glu Gln Arg Gln Ala Trp Glu Ala Arg Tyr Ala Glu Ser Glu Arg
 410 415 420
 cgc ttc acc gct cac acc gct cag atc gag cgt cgt cgt cag cag gct 1411
 Arg Phe Thr Ala His Thr Ala Gln Ile Glu Arg Arg Arg Gln Gln Ala
 425 430 435
 gaa gag gca gct gcc gag gct ccg gcc ggc aac tac tcc act gat tct 1459
 Glu Glu Ala Ala Ala Glu Ala Pro Ala Gly Asn Tyr Ser Thr Asp Ser
 440 445 450
 gca gaa gat gca cct gca gca gaa gca gtt gaa gag tcc gct ggc tcc 1507
 Ala Glu Asp Ala Pro Ala Glu Ala Val Glu Ser Ala Gly Ser
 455 460 465
 ctc gct tcc gat gag cag ctc gct gct ctt cgc gag aag ctc gca ggt 1555
 Leu Ala Ser Asp Glu Gln Leu Ala Ala Leu Arg Glu Lys Leu Ala Gly
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 Asn

<210> 356

<211> 486

<212> PRT

<213> Corynebacterium glutamicum

<400> 356

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 1 5 10 15
 Ala Glu Asp Phe Leu Ala Ala Ile Asp Ala Thr Ile Lys Tyr Phe Asn
 20 25 30
 Asp Gly Asp Ile Val Glu Gly Thr Val Val Lys Val Asp Arg Asp Glu
 35 40 45
 Val Leu Leu Asp Ile Gly Tyr Lys Thr Glu Gly Val Ile Pro Ser Arg
 50 55 60
 Glu Leu Ser Ile Lys His Asp Val Asp Pro Asp Glu Val Val Glu Val
 65 70 75 80
 Gly Asp Gln Ile Asp Ala Leu Val Leu Thr Lys Glu Asp Lys Glu Gly
 85 90 95
 Arg Leu Ile Leu Ser Lys Lys Arg Ala Gln Tyr Glu Arg Ala Trp Gly
 100 105 110
 Ala Ile Glu Glu Leu Lys Glu Lys Asp Glu Pro Val Thr Gly Thr Val
 115 120 125
 Ile Glu Val Val Lys Gly Gly Leu Ile Ile Asp Ile Gly Leu Arg Gly
 130 135 140

Phe Leu Pro Ala Ser Leu Val Glu Met Arg Arg Val Arg Asp Leu Asp
145 150 155 160

Pro Tyr Ile Gly Gln Glu Leu Glu Ala Lys Ile Ile Glu Leu Asp Lys
165 170 175

Asn Arg Asn Asn Val Val Leu Ser Arg Arg Ala Phe Leu Glu Gln Thr
180 185 190

Gln Ser Glu Val Arg Ser Glu Phe Leu His Gln Leu Gln Lys Gly Gln
195 200 205

Val Arg Lys Gly Val Val Ser Ser Ile Val Asn Phe Gly Ala Phe Val
210 215 220

Asp Leu Gly Gly Val Asp Gly Leu Val His Val Ser Glu Leu Ser Trp
225 230 235 240

Lys His Ile Asp His Pro Ser Glu Val Val Thr Val Gly Asp Glu Val
245 250 255

Thr Val Glu Val Leu Glu Val Asp Leu Asp Arg Glu Arg Val Ser Leu
260 265 270

Ser Leu Lys Ala Thr Gln Glu Asp Pro Trp Arg Val Phe Ala Arg Thr
275 280 285

His Ala Val Gly Gln Ile Val Pro Gly Lys Val Thr Lys Leu Val Pro
290 295 300

Phe Gly Ala Phe Val Arg Val Glu Glu Gly Ile Glu Gly Leu Val His
305 310 315 320

Ile Ser Glu Leu Ala Gln Arg His Val Glu Val Pro Asp Gln Val Val
325 330 335

Ala Val Gly Glu Glu Val Met Val Lys Val Ile Asp Ile Asp Leu Glu
340 345 350

Arg Arg Arg Ile Ser Leu Ser Leu Lys Gln Ala Asp Glu Asp Tyr Thr
355 360 365

Glu Glu Phe Asp Pro Ser Lys Tyr Gly Met Ala Asp Ser Tyr Asp Glu
370 375 380

Gln Gly Asn Tyr Ile Phe Pro Glu Gly Phe Asp Ala Glu Thr Asn Glu
385 390 395 400

Trp Leu Glu Gly Phe Asp Glu Gln Arg Gln Ala Trp Glu Ala Arg Tyr
405 410 415

Ala Glu Ser Glu Arg Arg Phe Thr Ala His Thr Ala Gln Ile Glu Arg
420 425 430

Arg Arg Gln Gln Ala Glu Glu Ala Ala Ala Glu Ala Pro Ala Gly Asn
435 440 445

Tyr Ser Thr Asp Ser Ala Glu Asp Ala Pro Ala Ala Glu Ala Val Glu
450 455 460

Glu Ser Ala Gly Ser Leu Ala Ser Asp Glu Gln Leu Ala Ala Leu Arg

465

470

475

480

Glu Lys Leu Ala Gly Asn
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<210> 357

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(838)

<223> RXN01912

<400> 357

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Met Arg Arg Phe Ile
1 5

ttc acc gag cgt aac ggc atc tac atc att gac ctt cag cag acc ctg 163
Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp Leu Gln Gln Thr Leu
10 15 20

acc tac atc gat cag gct ttc gag ttc gtc aag gaa acc gtt gct cac 211
Thr Tyr Ile Asp Gln Ala Phe Glu Phe Val Lys Glu Thr Val Ala His
25 30 35

ggt ggc acc gtt ctt ttc gtt ggt acc aaa aag cag gct cag gaa gct 259
Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys Gln Ala Gln Glu Ala
40 45 50

gtt cag gtt gag gca gac cgc gtt ggt atg cct tac gtg aac cac cgt 307
Val Gln Val Glu Ala Asp Arg Val Gly Met Pro Tyr Val Asn His Arg
55 60 65

tgg ctc ggc ggc atg ctg acc aac ttc cag acc gtt tcc aag cgt ctg 355
Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr Val Ser Lys Arg Leu
70 75 80 85

aac cgc atg aag gaa ctg cag gca atg gat gct gca gaa aac ggc tac 403
Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala Ala Glu Asn Gly Tyr
90 95 100

gag ggt cgc acc aag cgc gaa gtt ctc atg ctg acc cgt gag cgc acc 451
Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu Thr Arg Glu Arg Thr
105 110 115

aag ctg gag cgc gtc ctc ggt ggt atc gca gag atg acc cgc gtg cct 499
Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu Met Thr Arg Val Pro
120 125 130

tcc gca ctg tgg atc att gac acc aac aag gag cac atc gct gtc gct 547
Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu His Ile Ala Val Ala
135 140 145

gag gct cac aag ctg aac atc cca gtt gtt gcc atc ctg gac acc aac 595
Glu Ala His Lys Leu Asn Ile Pro Val Val Ala Ile Leu Asp Thr Asn

150	155	160	165	
tgt gac cca gac gtt gtt gac ttc cca gtt cct ggt aac gac gac gca				643
Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro Gly Asn Asp Asp Ala				
170		175	180	
atc cgc tcc acc gca ctg ctt tcc cgc gtt atc tcc acc gct gtg gaa				691
Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile Ser Thr Ala Val Glu				
185	190	195		
gag ggt aag aag gca cgc gag gag cgt cag ctg gca gct gct aag gat				739
Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu Ala Ala Ala Lys Asp				
200	205	210		
gca gca ggc gac gca aag cct gag gca gag gaa gca cca gca gca gct				787
Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu Ala Pro Ala Ala Ala				
215	220	225		
gag gct gaa gag gca cct gca gct gag gct gaa gag gca cct gca gct				835
Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu Glu Ala Pro Ala Ala				
230	235	240	245	
gag taagctgccc ttaactgcag ttt				861
Glu				

<210> 358

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

Met Arg Arg Phe Ile Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp				
1	5	10	15	
Leu Gln Gln Thr Leu Thr Tyr Ile Asp Gln Ala Phe Glu Phe Val Lys				
20	25	30		
Glu Thr Val Ala His Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys				
35	40	45		
Gln Ala Gln Glu Ala Val Gln Val Glu Ala Asp Arg Val Gly Met Pro				
50	55	60		
Tyr Val Asn His Arg Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr				
65	70	75	80	
Val Ser Lys Arg Leu Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala				
85	90	95		
Ala Glu Asn Gly Tyr Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu				
100	105	110		
Thr Arg Glu Arg Thr Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu				
115	120	125		
Met Thr Arg Val Pro Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu				
130	135	140		
His Ile Ala Val Ala Glu Ala His Lys Leu Asn Ile Pro Val Val Ala				

145	150	155	160
Ile Leu Asp Thr Asn Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro	165	170	175
Gly Asn Asp Asp Ala Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile	180	185	190
Ser Thr Ala Val Glu Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu	195	200	205
Ala Ala Ala Lys Asp Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu	210	215	220
Ala Pro Ala Ala Ala Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu	225	230	235
Glu Ala Pro Ala Ala Glu	245		

<210> 359
 <211> 894
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(871)
 <223> FRXA01912

<400> 359
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 gtgtgcactt tgccaccaga cccgccgctg gaacccaaag atg cgt cgt ttc atc 115
 Met Arg Arg Phe Ile
 1 5
 ttc acc gag cgt aac ggc atc tac atc att gac ctt cag cag acc ctg 163
 Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp Leu Gln Gln Thr Leu
 10 15 20
 acc tac atc gat cag gct ttc gag ttc gtc aag gaa acc gtt gct cac 211
 Thr Tyr Ile Asp Gln Ala Phe Glu Phe Val Lys Glu Thr Val Ala His
 25 30 35
 ggt ggc acc gtt ctt ttc gtt ggt acc aaa aag cag gct cag gaa gct 259
 Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys Gln Ala Gln Glu Ala
 40 45 50
 gtt cag gtt gag gca gac cgc gtt ggt atg cct tac gtg aac cac cgt 307
 Val Gln Val Glu Ala Asp Arg Val Gly Met Pro Tyr Val Asn His Arg
 55 60 65
 tgg ctc ggc ggc atg ctg acc aac ttc cag acc gtt tcc aag cgt ctg 355
 Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr Val Ser Lys Arg Leu
 70 75 80 85
 aac cgc atg aag gaa ctg cag gca atg gat gct gca gaa aac ggc tac 403
 Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala Ala Glu Asn Gly Tyr
 90 95 100

<400> 360
Met Arg Arg Phe Ile Phe Thr Glu Arg Asn Gly Ile Tyr Ile Ile Asp
1 5 10 15
Leu Gln Gln Thr Leu Thr Tyr Ile Asp Gln Ala Phe Glu Phe Val Lys
20 25 30
Glu Thr Val Ala His Gly Gly Thr Val Leu Phe Val Gly Thr Lys Lys
35 40 45
Gln Ala Gln Glu Ala Val Gln Val Glu Ala Asp Arg Val Gly Met Pro
50 55 60

Tyr Val Asn His Arg Trp Leu Gly Gly Met Leu Thr Asn Phe Gln Thr
 65 70 75 80
 Val Ser Lys Arg Leu Asn Arg Met Lys Glu Leu Gln Ala Met Asp Ala
 85 90 95
 Ala Glu Asn Gly Tyr Glu Gly Arg Thr Lys Arg Glu Val Leu Met Leu
 100 105 110
 Thr Arg Glu Arg Thr Lys Leu Glu Arg Val Leu Gly Gly Ile Ala Glu
 115 120 125
 Met Thr Arg Val Pro Ser Ala Leu Trp Ile Ile Asp Thr Asn Lys Glu
 130 135 140
 His Ile Ala Val Ala Glu Ala His Lys Leu Asn Ile Pro Val Val Ala
 145 150 155 160
 Ile Leu Asp Thr Asn Cys Asp Pro Asp Val Val Asp Phe Pro Val Pro
 165 170 175
 Gly Asn Asp Asp Ala Ile Arg Ser Thr Ala Leu Leu Ser Arg Val Ile
 180 185 190
 Ser Thr Ala Val Glu Glu Gly Lys Lys Ala Arg Glu Glu Arg Gln Leu
 195 200 205
 Ala Ala Ala Lys Asp Ala Ala Gly Asp Ala Lys Pro Glu Ala Glu Glu
 210 215 220
 Ala Pro Ala Ala Ala Glu Ala Glu Glu Ala Pro Ala Ala Glu Ala Glu
 225 230 235 240
 Glu His Leu Gln Leu Ser Lys Leu Pro Leu Thr Ala Val Ser Ala Val
 245 250 255

Ser

<210> 361
 <211> 737
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(714)
 <223> RXA02041

<400> 361
 cgt ttg ggc atc act tcc gac tgg aag tcc cat tgg tac gcc gac aag 48
 Arg Leu Gly Ile Thr Ser Asp Trp Lys Ser His Trp Tyr Ala Asp Lys
 1 5 10 15
 tct tac gct gac tac gtc gca gaa gac atc aag att cgc gaa ttc ctg 96
 Ser Tyr Ala Asp Tyr Val Ala Glu Asp Ile Lys Ile Arg Glu Phe Leu
 20 25 30
 tcc aag ggc ctc gac cgt gcc ggc atc gcc gac gtc gtc atc gag cgc 144

Ser Lys Gly Leu Asp Arg Ala Gly Ile Ala Asp Val Val Ile Glu Arg
 35 40 45
 acc cgc gac cgc gtt cgc gta gac atc cac acc gct cgc cca ggc atc 192
 Thr Arg Asp Arg Val Arg Val Asp Ile His Thr Ala Arg Pro Gly Ile
 50 55 60
 gtc att ggt cgt cgt ggc gct gag gct gac cgc atc cgc cgt gag ctc 240
 Val Ile Gly Arg Arg Gly Ala Glu Ala Asp Arg Ile Arg Arg Glu Leu
 65 70 75 80
 gag aag ctc acc ggc aag cag gtt gcc ctc aac atc ctc gag gtc aag 288
 Glu Lys Leu Thr Gly Lys Gln Val Ala Leu Asn Ile Leu Glu Val Lys
 85 90 95
 aac gtc gat gct aac gct aag ctg gtg gca cag tcc atc gct gag cag 336
 Asn Val Asp Ala Asn Ala Lys Leu Val Ala Gln Ser Ile Ala Glu Gln
 100 105 110
 ctg acc aac cgc gtg gca ttc cgt cgc gca atg cgc aag gct atc cag 384
 Leu Thr Asn Arg Val Ala Phe Arg Arg Ala Met Arg Lys Ala Ile Gln
 115 120 125
 tct gca atg cgt cag cca cag gtt aag ggc atc aag gtc gtg tgc tcc 432
 Ser Ala Met Arg Gln Pro Gln Val Lys Gly Ile Lys Val Val Cys Ser
 130 135 140
 ggt cgt ctc ggc ggt gcc gag atg tcc cgc acc gag cgc tac cac gaa 480
 Gly Arg Leu Gly Gly Ala Glu Met Ser Arg Thr Glu Arg Tyr His Glu
 145 150 155 160
 ggt cgc gtt cca ctg cac acc ctt cgc gca gaa atc gat tac ggc acc 528
 Gly Arg Val Pro Leu His Thr Leu Arg Ala Glu Ile Asp Tyr Gly Thr
 165 170 175
 tac gag gct cac acc act ttc gga cgc atc ggc gtc aag gtg tgg atc 576
 Tyr Glu Ala His Thr Thr Phe Gly Arg Ile Gly Val Lys Val Trp Ile
 180 185 190
 tac aag ggt gac gtc gtt ggt gga cgt cgc gag agc gag atc aat gca 624
 Tyr Lys Gly Asp Val Val Gly Gly Arg Arg Glu Ser Glu Ile Asn Ala
 195 200 205
 ccc gca gag cgt cgc ggc cgc ggc gac cgc aac gca cgt ccg cgt cgt 672
 Pro Ala Glu Arg Arg Gly Arg Gly Asp Arg Asn Ala Arg Pro Arg Arg
 210 215 220
 ggt ggc cag cgt cgt cag cgt gct gag cag aag cag gag ggc 714
 Gly Gly Gln Arg Arg Gln Arg Ala Glu Gln Lys Gln Glu Gly
 225 230 235
 taaacatgct tattcctaag cgc 737

<210> 362

<211> 238

<212> PRT

<213> Corynebacterium glutamicum

<400> 362

Arg Leu Gly Ile Thr Ser Asp Trp Lys Ser His Trp Tyr Ala Asp Lys

1	5	10	15
Ser Tyr Ala Asp	Tyr Val Ala Glu	Asp Ile Lys Ile Arg	Glu Phe Leu
20		25	30
Ser Lys Gly Leu	Asp Arg Ala Gly	Ile Ala Asp Val	Val Ile Glu Arg
35		40	45
Thr Arg Asp Arg	Val Arg Val Asp	Ile His Thr Ala	Arg Pro Gly Ile
50		55	60
Val Ile Gly Arg	Arg Gly Ala Glu	Ala Asp Arg Ile	Arg Arg Glu Leu
65		70	75
Glu Lys Leu Thr	Gly Lys Gln Val	Ala Leu Asn Ile	Leu Glu Val Lys
	85	90	95
Asn Val Asp Ala	Asn Ala Lys Leu	Val Ala Gln Ser	Ile Ala Glu Gln
	100	105	110
Leu Thr Asn Arg	Val Ala Phe Arg	Arg Ala Met Arg	Lys Ala Ile Gln
	115	120	125
Ser Ala Met Arg	Gln Pro Gln Val	Lys Gly Ile Lys	Val Val Cys Ser
	130	135	140
Gly Arg Leu Gly	Gly Ala Glu Met	Ser Arg Thr Glu	Arg Tyr His Glu
145		150	155
Gly Arg Val Pro	Leu His Thr Leu	Arg Ala Glu Ile	Asp Tyr Gly Thr
	165	170	175
Tyr Glu Ala His	Thr Thr Phe Gly	Arg Ile Gly Val	Lys Val Trp Ile
	180	185	190
Tyr Lys Gly Asp	Val Val Gly Gly	Arg Arg Glu Ser	Glu Ile Asn Ala
	195	200	205
Pro Ala Glu Arg	Arg Gly Arg Gly	Asp Arg Asn Ala	Arg Pro Arg Arg
	210	215	220
Gly Gly Gln Arg	Arg Gln Arg Ala	Glu Gln Lys Gln	Glu Gly
225		230	235

<210> 363

<211> 726

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> RXA00672

<400> 363

tggagatcgg ttcaatctcc gacgtgaccc cacagccaca caacggctgc cgtccaccaa 60

agcgctcgctg cggttaatat ggaaggaaag gtaatacaaaa atg gct cgt tat acc 115

Met Ala Arg Tyr Thr

1

5

ggc cca gca acc cgt aaa tcc cgt cgt ctg cgc gtc gac ctt gtt ggt 163
Gly Pro Ala Thr Arg Lys Ser Arg Arg Leu Arg Val Asp Leu Val Gly
10 15 20

gga gac atg gcg ttt gag cgc cgt cct tac cct cca gga cag gca ggc 211
Gly Asp Met Ala Phe Glu Arg Arg Pro Tyr Pro Pro Gly Gln Ala Gly
25 30 35

cgt gca cgc atc aag gag tcc gag tac ctg ctg cag ctc cag gag aag 259
Arg Ala Arg Ile Lys Glu Ser Glu Tyr Leu Leu Gln Leu Gln Glu Lys
40 45 50

cag aag gct cgt ttc atc tac ggc gtc atg gaa aag cag ttc cgt cgt 307
Gln Lys Ala Arg Phe Ile Tyr Gly Val Met Glu Lys Gln Phe Arg Arg
55 60 65

tac tac gcc gag gct aac cgt cgc gca ggc aag acc ggt gag aac ctg 355
Tyr Tyr Ala Glu Ala Asn Arg Arg Ala Gly Lys Thr Gly Glu Asn Leu
70 75 80 85

gtc gtc ctg ctc gag tcc cgc ctc gac aac gtc gtg tac cgc gca ggt 403
Val Val Leu Leu Glu Ser Arg Leu Asp Asn Val Val Tyr Arg Ala Gly
90 95 100

ctg gca aac acc cgt cgc cag gct cgt cag ctt gtt tcc cac ggt cac 451
Leu Ala Asn Thr Arg Arg Gln Ala Arg Gln Leu Val Ser His Gly His
105 110 115

ttc acc gtg aac ggc aag gca atc gac gtt cca tct ttc cgc gtt tct 499
Phe Thr Val Asn Gly Lys Ala Ile Asp Val Pro Ser Phe Arg Val Ser
120 125 130

cag tac gac atc atc aat gtt cgt gag aag tcc cag aag atg aac tgg 547
Gln Tyr Asp Ile Ile Asn Val Arg Glu Lys Ser Gln Lys Met Asn Trp
135 140 145

ttc gaa gag gct cag gac aac ctg gcc gac gca gtc gtc cca gct tgg 595
Phe Glu Glu Ala Gln Asp Asn Leu Ala Asp Ala Val Val Pro Ala Trp
150 155 160 165

ctc cag gtc gtt cct gag aac ctt cgt atc ctc gtg cac cag ctc cca 643
Leu Gln Val Val Glu Asn Leu Arg Ile Leu Val His Gln Leu Pro
170 175 180

gag cgc gca cag atc gat atc cca ctg caa gag cag ctc atc gtc gag 691
Glu Arg Ala Gln Ile Asp Ile Pro Leu Gln Glu Gln Leu Ile Val Glu
185 190 195

ttc tac tcg aag tagtttttgc ttaccggct gcc 726
Phe Tyr Ser Lys
200

<210> 364

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

Met Ala Arg Tyr Thr Gly Pro Ala Thr Arg Lys Ser Arg Arg Leu Arg

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<210> 365
<211> 756
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(733)  
<223> RXA00697
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<400> 365
taccacggcc gcgttgccagc tctcgctgac gccgctcgtg aaggtgggtct gaaattctaa 60

tgatgaccat ttctaagaac atcaacggaa ggattgcgta atg ccg gga cgt gaa 115
                               Met Pro Gly Arg Glu
                               1           5

cgg cgt gac ggc gga cgc tcc gcc gac gac aac aag caa aac gat cgc 163
Arg Arg Asp Gly Gly Arg Ser Ala Asp Asp Asn Lys Gln Asn Asp Arg
                10                15                20

aac gaq cgt cgt qqc gga qqc cqc cqc qat qac cqt cqc aat cag cag 211

```

<400> 366
Met Pro Gly Arg Glu Arg Arg Asp Gly Gly Arg Ser Ala Asp Asp Asn
1 5 10 15
Lys Gln Asn Asp Arg Asn Glu Arg Arg Gly Gly Gly Arg Arg Asp Asp
20 25 30

```

<400> 367
gctgacgcaa cgaccctcct gctatgccaa cgacggcatg gccgaaaaaa caattactag \60

accataggag gtgatgaggt ccgtgcgtca atacgaactt atg atc att ctc gat 115
                                         Met Ile Ile Leu Asp
                                         1             5

cct tct cag gat gag cgc act gtt gcc ccg tcc ctg gat aaa ttc ctc 163
Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser Leu Asp Lys Phe Leu
                        10                      15                      20

gag gtt gtc cgc aag gac aag ggt gac gtt gtg aag gtt gat gtt tgg 211
Glu Val Val Arg Lys Asp Lys Gly Asp Val Val Lys Val Asp Val Trp

```

```
<210> 368
<211> 89
<212> PRT
<213> Corynebacterium glutamicum
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```

<400> 368
Met Ile Ile Leu Asp Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser
  1           5          10          15
Leu Asp Lys Phe Leu Glu Val Val Arg Lys Asp Lys Gly Asp Val Val
      20          25          30
Lys Val Asp Val Trp Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys
      35          40          45
Lys Glu Glu Gly Val Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala
      50          55          60
Thr Val Leu Glu Leu Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu
      65          70          75          80
Arg Thr Lys Val Leu Arg Leu Asp Lys
      85

```

```
<210> 369
<211> 355
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(355)
<223> FRXA00545
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<400> 369
gctgacgcaa cgaccctcct gctatgccaa cgacggcatg gccgaaaaaa caattactag 60

accataggag gtgatgaggt ccgatgcgtca atacgaactt atg atc att ctc gat 115
               Met Ile Ile Leu Asp
                1             5

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cct tct cag gat gag cgc act gtt gcc ccg tcc ctg gat aaa ttc ctc 163
Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser Leu Asp Lys Phe Leu
10 15 20

gag gtt gtc cgc aag gac aag ggt gac gtt gtg aag gtt gat gtt tgg 211
Glu Val Val Arg Lys Asp Lys Gly Asp Val Val Lys Val Asp Val Trp
25 30 35

ggc aag cgc cgt ctt gca tac cca atc gac aag aag gaa gag ggc gtt 259
Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys Lys Glu Glu Gly Val
40 45 50

tac gcc gtc gtc gat ctc aag tgt gag tct gcg acc gta ctc gag ctc 307
Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala Thr Val Leu Glu Leu
55 60 65

gat cgt gtt ctg aac ctg aat gat ggt gtc ctg cgc acc aag gtt ctg 355
Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu Arg Thr Lys Val Leu
70 75 80 85

<210> 370

<211> 85

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

Met Ile Ile Leu Asp Pro Ser Gln Asp Glu Arg Thr Val Ala Pro Ser
1 5 10 15

Leu Asp Lys Phe Leu Glu Val Val Arg Lys Asp Lys Gly Asp Val Val
20 25 30

Lys Val Asp Val Trp Gly Lys Arg Arg Leu Ala Tyr Pro Ile Asp Lys
35 40 45

Lys Glu Glu Gly Val Tyr Ala Val Val Asp Leu Lys Cys Glu Ser Ala
50 55 60

Thr Val Leu Glu Leu Asp Arg Val Leu Asn Leu Asn Asp Gly Val Leu
65 70 75 80

Arg Thr Lys Val Leu
85

<210> 371

<211> 588

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(565)

<223> RXA01279

<400> 371

tgtccggttac aagatcggtc gtggcgcaact ggatacccag ggtggttaagg accgcaagca 60

ggctcggttcc cgctacggcg cgaagagggg ataattaaaa atg cgt aaa tca gca 115
Met Arg Lys Ser Ala

Leu Gly Asn Val Arg Pro Asp Leu Glu Val Arg Ser Arg Arg Val Gly
 65 70 75 80
 Gly Ala Thr Tyr Gln Val Pro Val Asp Val Arg Pro Glu Arg Ala Asn
 85 90 95
 Thr Leu Ala Leu Arg Trp Leu Val Thr Phe Thr Arg Gln Arg Arg Glu
 100 105 110
 Asn Thr Met Ile Glu Arg Leu Ala Asn Glu Leu Leu Asp Ala Ala Asn
 115 120 125
 Gly Leu Gly Ala Ser Val Lys Arg Arg Glu Asp Thr His Lys Met Ala
 130 135 140
 Glu Ala Asn Arg Ala Phe Ala His Tyr Arg Trp
 145 150 155

<210> 373
 <211> 519
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(496)
 <223> RXA00694

<400> 373
 cgactattga gttcgggtgag cgttgagtgg ccagaaaaca cacgggtaac gtccaagggtg 60
 ggaaggggaac cccaacgaga aaggcatcag gtcgtctcta atg aca atg act gat 115
 Met Thr Met Thr Asp
 1 5
 cca atc gcc gac atg ctg tcg cgc gtg cgc aat gct agc aat gcg cac 163
 Pro Ile Ala Asp Met Leu Ser Arg Val Arg Asn Ala Ser Asn Ala His
 10 15 20
 cac gac acc gtg tcc atg cca tcc tcc aag atc aag gca aac atc gcc 211
 His Asp Thr Val Ser Met Pro Ser Ser Lys Ile Lys Ala Asn Ile Ala
 25 30 35
 gag atc ttg aag cag gaa ggc tac atc gct aac tac acc gtt gag gat 259
 Glu Ile Leu Lys Gln Glu Gly Tyr Ile Ala Asn Tyr Thr Val Glu Asp
 40 45 50
 gca aag gtc ggc aag acc ctg tcc ctc gag ctg aag tac agc aac acc 307
 Ala Lys Val Gly Lys Thr Leu Ser Leu Glu Leu Lys Tyr Ser Asn Thr
 55 60 65
 cgt gag cgc tcc atc gct ggt ctg cgc cgc gtt tcc aag cct ggt ctg 355
 Arg Glu Arg Ser Ile Ala Gly Leu Arg Arg Val Ser Lys Pro Gly Leu
 70 75 80 85
 cgt gta tac gct aag tcc acc aat ctg cca cag gtt ctg ggc ggc ctt 403
 Arg Val Tyr Ala Lys Ser Thr Asn Leu Pro Gln Val Leu Gly Gly Leu
 90 95 100
 ggc gtg gct atc att tcc acg tca cag ggc ctc ctg acc gac cgt cag 451

Gly Val Ala Ile Ile Ser Thr Ser Gln Gly Leu Leu Thr Asp Arg Gln
 105 110 115

gct acc gag aag ggc gta ggc gga gaa gtc ctc gcc tac gtc tgg 496
 Ala Thr Glu Lys Gly Val Gly Gly Glu Val Leu Ala Tyr Val Trp
 120 125 130

taatagggag gattgactaa ata 519

<210> 374

<211> 132

<212> PRT

<213> Corynebacterium glutamicum

<400> 374

Met Thr Met Thr Asp Pro Ile Ala Asp Met Leu Ser Arg Val Arg Asn
 1 5 10 15

Ala Ser Asn Ala His His Asp Thr Val Ser Met Pro Ser Ser Lys Ile
 20 25 30

Lys Ala Asn Ile Ala Glu Ile Leu Lys Gln Glu Gly Tyr Ile Ala Asn
 35 40 45

Tyr Thr Val Glu Asp Ala Lys Val Gly Lys Thr Leu Ser Leu Glu Leu
 50 55 60

Lys Tyr Ser Asn Thr Arg Glu Arg Ser Ile Ala Gly Leu Arg Arg Val
 65 70 75 80

Ser Lys Pro Gly Leu Arg Val Tyr Ala Lys Ser Thr Asn Leu Pro Gln
 85 90 95

Val Leu Gly Gly Leu Gly Val Ala Ile Ile Ser Thr Ser Gln Gly Leu
 100 105 110

Leu Thr Asp Arg Gln Ala Thr Glu Lys Gly Val Gly Gly Glu Val Leu
 115 120 125

Ala Tyr Val Trp
 130

<210> 375

<211> 492

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(469)

<223> RXN02038

<400> 375

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agaagcctga ggcctacgag atcaagaagg tggcccagta atg tca gag cct atc 115
 Met Ser Glu Pro Ile
 1 5

cag aac gag aac gta gag agc aac gtc gca gac gct gct gac atc gct 163
 Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp Ala Ala Asp Ile Ala
 10 15 20

gca gca acc gct gca acc gag gag ttc acc aac acc atc ggc gat gca 211
 Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn Thr Ile Gly Asp Ala
 25 30 35

att gct act gct tcc gaa gaa gag acc atc gag gct gca cca gta gta 259
 Ile Ala Thr Ala Ser Glu Glu Glu Thr Ile Glu Ala Ala Pro Val Val
 40 45 50

ctc gac ggc cca atc cag acc gtt ggt cgc cgt aag cgc gcc atc gtt 307
 Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg Lys Arg Ala Ile Val
 55 60 65

cgc gtc cgc ctt gta gct ggc tcc ggc gag ttc aag tgc aac ggt cgc 355
 Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe Lys Cys Asn Gly Arg
 70 75 80 85

acc ctg gaa gag tac ttc cct aac aag ctg cac cag cag ctg atc aag 403
 Thr Leu Glu Glu Tyr Phe Pro Asn Lys Leu His Gln Gln Leu Ile Lys
 90 95 100

gct cct ttg gtc ctt ctg gac cgc ctg aac caa tgc aac atc gag gct 451
 Ala Pro Leu Val Leu Leu Asp Arg Leu Asn Gln Cys Asn Ile Glu Ala
 105 110 115

tct ata aag gga cct aaa tagatcggcc aggttatggc aat 492
 Ser Ile Lys Gly Pro Lys
 120

<210> 376

<211> 123

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

Met Ser Glu Pro Ile Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp
 1 5 10 15

Ala Ala Asp Ile Ala Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn
 20 25 30

Thr Ile Gly Asp Ala Ile Ala Thr Ala Ser Glu Glu Glu Thr Ile Glu
 35 40 45

Ala Ala Pro Val Val Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg
 50 55 60

Lys Arg Ala Ile Val Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe
 65 70 75 80

Lys Cys Asn Gly Arg Thr Leu Glu Glu Tyr Phe Pro Asn Lys Leu His
 85 90 95

Gln Gln Leu Ile Lys Ala Pro Leu Val Leu Leu Asp Arg Leu Asn Gln
 100 105 110

Cys Asn Ile Glu Ala Ser Ile Lys Gly Pro Lys

115

120

<210> 377
<211> 409
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(409)
<223> FRXA02038

<400> 377
ctgctgcttc cgcaaagaag ctgcacgttt tctccggctc cgagcaccca tacgtgctc 60
agaagcctga ggcctacgag atcaagaagg tggcccagta atg tca gag cct atc 115
Met Ser Glu Pro Ile
1 5
cag aac gag aac gta gag agc aac gtc gca gac gct gct gac atc gct 163
Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp Ala Ala Asp Ile Ala
10 15 20
gca gca acc gct gca acc gag gag ttc acc aac acc atc ggc gat gca 211
Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn Thr Ile Gly Asp Ala
25 30 35
att gct act gct tcc gaa gaa gag acc atc gag gct gca cca gta gta 259
Ile Ala Thr Ala Ser Glu Glu Glu Thr Ile Glu Ala Ala Pro Val Val
40 45 50
ctc gac ggc cca atc cag acc gtt ggt cgc cgt aag cgc gcc atc gtt 307
Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg Lys Arg Ala Ile Val
55 60 65
cgc gtc cgc ctt gta gct ggc tcc ggc gag ttc aag tgc aac ggt cgc 355
Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe Lys Cys Asn Gly Arg
70 75 80 85
acc ctg gaa gag tac ttc cct aac aag ctg cac cag cag ctg atc aag 403
Thr Leu Glu Glu Tyr Phe Pro Asn Lys Leu His Gln Gln Leu Ile Lys
90 95 100
gct cct 409
Ala Pro

<210> 378
<211> 103
<212> PRT
<213> Corynebacterium glutamicum

<400> 378
Met Ser Glu Pro Ile Gln Asn Glu Asn Val Glu Ser Asn Val Ala Asp
1 5 10 15
Ala Ala Asp Ile Ala Ala Ala Thr Ala Ala Thr Glu Glu Phe Thr Asn
20 25 30

Thr Ile Gly Asp Ala Ile Ala Thr Ala Ser Glu Glu Glu Thr Ile Glu
 35 40 45
 Ala Ala Pro Val Val Leu Asp Gly Pro Ile Gln Thr Val Gly Arg Arg
 50 55 60
 Lys Arg Ala Ile Val Arg Val Arg Leu Val Ala Gly Ser Gly Glu Phe
 65 70 75 80
 Lys Cys Asn Gly Arg Thr Leu Glu Glu Tyr Phe Pro Asn Lys Leu His
 85 90 95
 Gln Gln Leu Ile Lys Ala Pro
 100

<210> 379
 <211> 426
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(403)
 <223> RXA01287

<400> 379
 cgagccccc aa gcccgacaa cgttatagag aaagaatgaa gcgaattccc accgcttttc 60
 caaaatggaa gatgtgggac gagcgaggaa gaggataagc gtg gcg gga caa aag 115
 Val Ala Gly Gln Lys
 1 5
 atc cgc att agg ctc aag gcc tac gac cac gaa gcg att gat gcg tct 163
 Ile Arg Ile Arg Leu Lys Ala Tyr Asp His Glu Ala Ile Asp Ala Ser
 10 15 20
 gca cgc aag atc gtt gag acg gtc acc cgt acg ggt gcc cga gtc gtt 211
 Ala Arg Lys Ile Val Glu Thr Val Thr Arg Thr Gly Ala Arg Val Val
 25 30 35
 gga ccg gtg cct ttg cct acc gaa aag aac gta tac gcc gtt att cgt 259
 Gly Pro Val Pro Leu Pro Thr Glu Lys Asn Val Tyr Ala Val Ile Arg
 40 45 50
 tct cca cat aag tac aag gac tct cgc gag cac ttc gag atg cgc act 307
 Ser Pro His Lys Tyr Lys Asp Ser Arg Glu His Phe Glu Met Arg Thr
 55 60 65
 cac aag cgc ctg atc gac atc ctc gac ccg acg ccg aag act gtt gat 355
 His Lys Arg Leu Ile Asp Ile Leu Asp Pro Thr Pro Lys Thr Val Asp
 70 75 80 85
 gcc ctt atg cgc atc gac ctt ccg gcc agc gtc gac gtg aac att cag 403
 Ala Leu Met Arg Ile Asp Leu Pro Ala Ser Val Asp Val Asn Ile Gln
 90 95 100
 tgatcgacgg aatttttggc agc 426

<210> 380

<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 380
Val Ala Gly Gln Lys Ile Arg Ile Arg Leu Lys Ala Tyr Asp His Glu
1 5 10 15
Ala Ile Asp Ala Ser Ala Arg Lys Ile Val Glu Thr Val Thr Arg Thr
20 25 30
Gly Ala Arg Val Val Gly Pro Val Pro Leu Pro Thr Glu Lys Asn Val
35 40 45
Tyr Ala Val Ile Arg Ser Pro His Lys Tyr Lys Asp Ser Arg Glu His
50 55 60
Phe Glu Met Arg Thr His Lys Arg Leu Ile Asp Ile Leu Asp Pro Thr
65 70 75 80
Pro Lys Thr Val Asp Ala Leu Met Arg Ile Asp Leu Pro Ala Ser Val
85 90 95
Asp Val Asn Ile Gln
100

<210> 381
<211> 113
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(90)
<223> RXA00673

<400> 381
ctt cag gct gca ggc ctg gag atc ggt tca atc tcc gac gtg acc cca 48
Leu Gln Ala Ala Gly Leu Glu Ile Gly Ser Ile Ser Asp Val Thr Pro
1 5 10 15
cag cca cac aac ggc tgc cgt cca cca aag cgt cgt cgc gtt 90
Gln Pro His Asn Gly Cys Arg Pro Pro Lys Arg Arg Arg Val
20 25 30
taatagggaa ggaaaggtaa tac 113

<210> 382
<211> 30
<212> PRT
<213> Corynebacterium glutamicum

<400> 382
Leu Gln Ala Ala Gly Leu Glu Ile Gly Ser Ile Ser Asp Val Thr Pro
1 5 10 15
Gln Pro His Asn Gly Cys Arg Pro Pro Lys Arg Arg Arg Val
20 25 30

Asp Lys Val Ala Thr Ala Ala Leu Lys Gly Ser Pro Gln Arg Arg Gly

<400> 385																												
cacc	cg	ta	ag	aaca	ag	cg	ca	aca	acc	cg	ga	ccgt	att	tcc	ctc	at	ga	ag	t	ac	ga	tcc	ag	t	60			
ag	tcc	g	ta	ag	cac	gt	c	ga	at	t	ccg	c	g	ag	ga	at	a	at	g	Met	g	ct	a	ag	a	ag	t	115
																	1	5										
aag	atc	gcc	aag	aac	gag	aag	cg	aag	gaa	atc	gtc	gcc	cg	tac	gcg						163							
Lys	Ile	Ala	Lys	Asn	Glu	Lys	Arg	Lys	Glu	Ile	Val	Ala	Arg	Tyr	Ala													
																	10	15	20									
gag	cgt	cg	gct	gag	ctc	aag	gca	att	atc	agt	aac	cca	aac	acc	tct						211							
Glu	Arg	Arg	Ala	Glu	Leu	Lys	Ala	Ile	Ile	Ser	Asn	Pro	Asn	Thr	Ser													
																	25	30	35									
gac	gag	gat	cgt	ctg	gat	gca	cag	ttc	gaa	ctg	aac	agc	cag	cca	cgt						259							
Asp	Glu	Asp	Arg	Leu	Asp	Ala	Gln	Phe	Glu	Leu	Asn	Ser	Gln	Pro	Arg													
																	40	45	50									
gat	gct	gct	gct	gtc	cg	gtt	cgt	aac	cg	gac	tca	cac	gat	gg	cg						307							
Asp	Ala	Ala	Ala	Val	Arg	Val	Arg	Asn	Arg	Asp	Ser	His	Asp	Gly	Arg													
																	55	60	65									
cca	cg	gg	tac	ctc	cgt	aag	ttc	gg	ctt	tcc	cgt	gtc	cgt	atg	cg						355							
Pro	Arg	Gly	Tyr	Leu	Arg	Lys	Phe	Gly	Leu	Ser	Arg	Val	Arg	Met	Arg													
																	70	75	80	85								
gag	atg	gct	cac	cgt	gg	gag	ctg	ccg	gg	gtt	cgt	aag	tcc	agc	tgg						403							
Glu	Met	Ala	His	Arg	Gly	Glu	Leu	Pro	Gly	Val	Arg	Lys	Ser	Ser	Trp													
																	90	95	100									

taagggagtt tttaccaatg aag

426

<210> 386

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 386

Met Ala Lys Lys Ser Lys Ile Ala Lys Asn Glu Lys Arg Lys Glu Ile
1 5 10 15

Val Ala Arg Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Ile Ser
20 25 30

Asn Pro Asn Thr Ser Asp Glu Asp Arg Leu Asp Ala Gln Phe Glu Leu
35 40 45

Asn Ser Gln Pro Arg Asp Ala Ala Ala Val Arg Val Arg Asn Arg Asp
50 55 60

Ser His Asp Gly Arg Pro Arg Gly Tyr Leu Arg Lys Phe Gly Leu Ser
65 70 75 80

Arg Val Arg Met Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Val
85 90 95

Arg Lys Ser Ser Trp
100

<210> 387

<211> 390

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(367)

<223> RXA01487

<400> 387

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aaatttttca tgcggactga aataactttt aggagacacc atg gct ctt act tct 115
Met Ala Leu Thr Ser
1 5

gag cag aag aag tcc atc ctt tcc gag ttc ggc ctc cac gag acc gac 163
Glu Gln Lys Lys Ser Ile Leu Ser Glu Phe Gly Leu His Glu Thr Asp
10 15 20

acc ggt tcc cca gaa gca cag atc gcg ctt ctg acc aac cgc atc aac 211
Thr Gly Ser Pro Glu Ala Gln Ile Ala Leu Leu Thr Asn Arg Ile Asn
25 30 35

aac ctc acc gag cac ctc aag ttc cac aag cac gat cac cac tcc cgt 259
Asn Leu Thr Glu His Leu Lys Phe His Lys His Asp His His Ser Arg
40 45 50

cgt ggt ctg ctg ctg ctc gtt ggt cgt cgt cgt ggt ctg ctg aag tac 307
 Arg Gly Leu Leu Leu Leu Val Gly Arg Arg Arg Gly Leu Leu Lys Tyr
 55 60 65
 ctg gct gac aac aac gtt gat cgc tac cgt gat ctg atc gca cgc ctc 355
 Leu Ala Asp Asn Asn Val Asp Arg Tyr Arg Asp Leu Ile Ala Arg Leu
 70 75 80 85
 ggc ctg cgt cga taagcctggt ttttccagtc ttt 390
 Gly Leu Arg Arg

<210> 388
 <211> 89
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 388
 Met Ala Leu Thr Ser Glu Gln Lys Lys Ser Ile Leu Ser Glu Phe Gly
 1 5 10 15
 Leu His Glu Thr Asp Thr Gly Ser Pro Glu Ala Gln Ile Ala Leu Leu
 20 25 30
 Thr Asn Arg Ile Asn Asn Leu Thr Glu His Leu Lys Phe His Lys His
 35 40 45
 Asp His His Ser Arg Arg Gly Leu Leu Leu Leu Val Gly Arg Arg Arg
 50 55 60
 Gly Leu Leu Lys Tyr Leu Ala Asp Asn Asn Val Asp Arg Tyr Arg Asp
 65 70 75 80
 Leu Ile Ala Arg Leu Gly Leu Arg Arg
 85

<210> 389
 <211> 618
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(595)
 <223> RXA02752

<400> 389
 ccggaggagt cacgcgcagg ttaaacaaga agggctgaac cggctcacca gcacacggtg 60
 agtgactgta ctgcccagtg acctagtgag gaaaattcac atg gct gta aag att 115
 Met Ala Val Lys Ile
 1 5
 aag ctc cag cgc ctc ggc aag atc cgt acc ccg cac tac cgc gtt gtc 163
 Lys Leu Gln Arg Leu Gly Lys Ile Arg Thr Pro His Tyr Arg Val Val
 10 15 20
 atc gct gat gca cgc acc aag cgc gac ggc aag gtt atc gag aac atc 211
 Ile Ala Asp Ala Arg Thr Lys Arg Asp Gly Lys Val Ile Glu Asn Ile

25	30	35	
ggt atc tac gag cca aag gct gag cct tcc gta atc aag atc aac tcc			259
Gly Ile Tyr Glu Pro Lys Ala Glu Pro Ser Val Ile Lys Ile Asn Ser			
40	45	50	
gag cgt gcg cag cac tgg ctc tcc gtt ggc gct cag cca acc gag gct			307
Glu Arg Ala Gln His Trp Leu Ser Val Gly Ala Gln Pro Thr Glu Ala			
55	60	65	
gtt gca gcg ctg ctc aag gtg acc ggc gac tgg cag aag ttc aag ggc			355
Val Ala Ala Leu Leu Lys Val Thr Gly Asp Trp Gln Lys Phe Lys Gly			
70	75	80	85
atc gag ggc gca gaa ggc acc ctc cgt gtt gca gag cct aag cca tcc			403
Ile Glu Gly Ala Glu Gly Thr Leu Arg Val Ala Glu Pro Lys Pro Ser			
90	95	100	
aag ctt gag ctg ttc aac cag gct ctt tct gag gct aac aac ggc cca			451
Lys Leu Glu Leu Phe Asn Gln Ala Leu Ser Glu Ala Asn Asn Gly Pro			
105	110	115	
acc gct gaa gcc atc act gaa aag aag aag aag gct cgc gag gac aag			499
Thr Ala Glu Ala Ile Thr Glu Lys Lys Lys Lys Ala Arg Glu Asp Lys			
120	125	130	
gaa gct aag gaa gca gct gag aag gct gct gct gaa aag gct gcc gct			547
Glu Ala Lys Glu Ala Ala Glu Lys Ala Ala Ala Glu Lys Ala Ala Ala			
135	140	145	
gca gag tcc gaa gag gct cca gct gag gaa gct gct gca gaa gag gca			595
Ala Glu Ser Glu Glu Ala Pro Ala Glu Glu Ala Ala Ala Glu Glu Ala			
150	155	160	165
taagccactt ttgtttgtac ttc			618

<210> 390

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 390

Met	Ala	Val	Lys	Ile	Lys	Leu	Gln	Arg	Leu	Gly	Lys	Ile	Arg	Thr	Pro
1				5					10					15	

His	Tyr	Arg	Val	Val	Ile	Ala	Asp	Ala	Arg	Thr	Lys	Arg	Asp	Gly	Lys
			20					25					30		

Val	Ile	Glu	Asn	Ile	Gly	Ile	Tyr	Glu	Pro	Lys	Ala	Glu	Pro	Ser	Val
		35				40						45			

Ile	Lys	Ile	Asn	Ser	Glu	Arg	Ala	Gln	His	Trp	Leu	Ser	Val	Gly	Ala
	50					55					60				

Gln	Pro	Thr	Glu	Ala	Val	Ala	Ala	Leu	Leu	Lys	Val	Thr	Gly	Asp	Trp
65					70					75					80

Gln	Lys	Phe	Lys	Gly	Ile	Glu	Gly	Ala	Glu	Gly	Thr	Leu	Arg	Val	Ala
				85					90					95	

Glu Pro Lys Pro Ser Lys Leu Glu Leu Phe Asn Gln Ala Leu Ser Glu
 100 105 110

Ala Asn Asn Gly Pro Thr Ala Glu Ala Ile Thr Glu Lys Lys Lys Lys
 115 120 125

Ala Arg Glu Asp Lys Glu Ala Lys Glu Ala Ala Glu Lys Ala Ala Ala
 130 135 140

Glu Lys Ala Ala Ala Ala Glu Ser Glu Glu Ala Pro Ala Glu Glu Ala
 145 150 155 160

Ala Ala Glu Glu Ala
 165

<210> 391
 <211> 384
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(361)
 <223> RXA02389

<400> 391
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tgtacacaac tttaactaga aagttcaaga ggtatttgcg atg gca aac atc aag 115
 Met Ala Asn Ile Lys
 1 5

tct cag atc aag cgt aac aag acc aac gag aag gct cgt ctg cgt aac 163
 Ser Gln Ile Lys Arg Asn Lys Thr Asn Glu Lys Ala Arg Leu Arg Asn
 10 15 20

cag gca gtt cgc tcc gca gtc cgc acc gag atc cgc aag ttc aac gct 211
 Gln Ala Val Arg Ser Ala Val Arg Thr Glu Ile Arg Lys Phe Asn Ala
 25 30 35

gcg att gaa gca ggc gac aag gat gca gct cag gct cag ctc cgt acc 259
 Ala Ile Glu Ala Gly Asp Lys Asp Ala Ala Gln Ala Gln Leu Arg Thr
 40 45 50

gct tcc cgc gca ctg gac aag gca gta acc aag ggt gtc ttc cac atc 307
 Ala Ser Arg Ala Leu Asp Lys Ala Val Thr Lys Gly Val Phe His Ile
 55 60 65

aac aac gct gct aac aag aag tcc aac atg gct acc gct ttc aac aag 355
 Asn Asn Ala Ala Asn Lys Lys Ser Asn Met Ala Thr Ala Phe Asn Lys
 70 75 80 85

ctt ggc taatttttgg ctcttttgaa aat 384
 Leu Gly

<210> 392
 <211> 87
 <212> PRT

<213> Corynebacterium glutamicum

<400> 392

Met Ala Asn Ile Lys Ser Gln Ile Lys Arg Asn Lys Thr Asn Glu Lys
1 5 10 15

Ala Arg Leu Arg Asn Gln Ala Val Arg Ser Ala Val Arg Thr Glu Ile
20 25 30

Arg Lys Phe Asn Ala Ala Ile Glu Ala Gly Asp Lys Asp Ala Ala Gln
35 40 45

Ala Gln Leu Arg Thr Ala Ser Arg Ala Leu Asp Lys Ala Val Thr Lys
50 55 60

Gly Val Phe His Ile Asn Asn Ala Ala Asn Lys Lys Ser Asn Met Ala
65 70 75 80

Thr Ala Phe Asn Lys Leu Gly
85

<210> 393

<211> 1137

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1114)

<223> RXA00671

<400> 393

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taccgacgtc aaatagcggg cgtcactcaa ggagagttca atg ctc att tca cag 115
Met Leu Ile Ser Gln
1 5

cgc cca acc atc acc gag gaa ttt gtt aat aac gca cgt tcc cgg ttt 163
Arg Pro Thr Ile Thr Glu Glu Phe Val Asn Asn Ala Arg Ser Arg Phe
10 15 20

gtc atc gag cca ctg gag cca ggt ttt ggc tac acc ctc ggt aac tcc 211
Val Ile Glu Pro Leu Glu Pro Gly Phe Gly Tyr Thr Leu Gly Asn Ser
25 30 35

ctg cgc cgt acc ctg ctg tcc tcc att cct gga gca gca gta acc agc 259
Leu Arg Arg Thr Leu Leu Ser Ser Ile Pro Gly Ala Ala Val Thr Ser
40 45 50

gtc aag att gac ggt gta ctc cac gag ttc acc acc atc agc ggt gtt 307
Val Lys Ile Asp Gly Val Leu His Glu Phe Thr Thr Ile Ser Gly Val
55 60 65

aag gaa gat gtc tct gac atc atc ttg aac atc aag gga ttg gtt ttg 355
Lys Glu Asp Val Ser Asp Ile Ile Leu Asn Ile Lys Gly Leu Val Leu
70 75 80 85

tct tct gat tcc gat gag cca gtt gtt atg cag ctg gtc aag gaa ggc 403
Ser Ser Asp Ser Asp Glu Pro Val Val Met Gln Leu Val Lys Glu Gly

90										95					100					
cca	gga	gtt	gta	act	gca	ggt	gac	att	cag	cca	cca	gca	ggc	gtg	gag	451				
Pro	Gly	Val	Val	Thr	Ala	Gly	Asp	Ile	Gln	Pro	Pro	Ala	Gly	Val	Glu					
105										110					115					
atc	cac	aac	ccg	gat	ctg	cac	att	gca	acc	ctg	aac	gag	acc	gcc	aag	499				
Ile	His	Asn	Pro	Asp	Leu	His	Ile	Ala	Thr	Leu	Asn	Glu	Thr	Ala	Lys					
120										125					130					
att	gag	atc	gag	ctc	atc	gtc	gag	cgt	gga	cgt	ggc	tac	gtt	ccc	gca	547				
Ile	Glu	Ile	Glu	Leu	Ile	Val	Glu	Arg	Gly	Arg	Gly	Tyr	Val	Pro	Ala					
135										140					145					
act	gtt	act	gca	acc	ggt	gga	gag	atc	ggc	cgc	att	ccg	gtc	gat	cag	595				
Thr	Val	Thr	Ala	Thr	Gly	Gly	Glu	Ile	Gly	Arg	Ile	Pro	Val	Asp	Gln					
150										155					160					165
atc	tac	tcc	cca	gta	ctg	aag	gtc	agc	tac	aag	gtt	gaa	gct	act	cgt	643				
Ile	Tyr	Ser	Pro	Val	Leu	Lys	Val	Ser	Tyr	Lys	Val	Glu	Ala	Thr	Arg					
170										175					180					
gtt	gag	cag	cgc	acc	gac	ttt	gac	aag	ctg	gtc	atc	gac	gtt	gag	acc	691				
Val	Glu	Gln	Arg	Thr	Asp	Phe	Asp	Lys	Leu	Val	Ile	Asp	Val	Glu	Thr					
185										190					195					
aag	aac	tct	att	acc	gca	cgt	gac	gcc	ctg	gcg	tcg	gca	ggt	aag	acc	739				
Lys	Asn	Ser	Ile	Thr	Ala	Arg	Asp	Ala	Leu	Ala	Ser	Ala	Gly	Lys	Thr					
200										205					210					
ctg	gtt	gag	ctg	ttc	ggc	ctc	gca	cgc	gag	ctg	aac	atc	gca	gcc	gag	787				
Leu	Val	Glu	Leu	Phe	Gly	Leu	Ala	Arg	Glu	Leu	Asn	Ile	Ala	Ala	Glu					
215										220					225					
ggc	atc	gag	atc	gga	cca	tct	cct	cag	gag	acc	gag	tac	atc	gct	gcc	835				
Gly	Ile	Glu	Ile	Gly	Pro	Ser	Pro	Gln	Glu	Thr	Glu	Tyr	Ile	Ala	Ala					
230										235					240					245
tac	agc	atg	cca	atc	gag	gat	ctg	gac	ttc	tct	gtc	cgt	tcc	tac	aac	883				
Tyr	Ser	Met	Pro	Ile	Glu	Asp	Leu	Asp	Phe	Ser	Val	Arg	Ser	Tyr	Asn					
250										255					260					
tgc	ctc	aag	cgc	gaa	gac	atc	cac	acc	gtg	ggt	gaa	ctc	gca	gag	cgc	931				
Cys	Leu	Lys	Arg	Glu	Asp	Ile	His	Thr	Val	Gly	Glu	Leu	Ala	Glu	Arg					
265										270					275					
gct	gag	tcc	gat	ttg	ctg	gat	atc	cgc	aac	ttc	gga	cag	aag	tcg	atc	979				
Ala	Glu	Ser	Asp	Leu	Leu	Asp	Ile	Arg	Asn	Phe	Gly	Gln	Lys	Ser	Ile					
280										285					290					
aac	gag	gta	aag	atc	aag	ctt	gct	ggc	ctg	ggt	ctg	acc	ctg	aag	gat	1027				
Asn	Glu	Val	Lys	Ile	Lys	Leu	Ala	Gly	Leu	Gly	Leu	Thr	Leu	Lys	Asp					
295										300					305					
gct	cct	gaa	gac	ttc	gat	cct	tca	act	ctt	gaa	ggt	tat	gac	gcc	gaa	1075				
Ala	Pro	Glu	Asp	Phe	Asp	Pro	Ser	Thr	Leu	Glu	Gly	Tyr	Asp	Ala	Glu					
310										315					320					325
act	ggt	ggc	tac	atc	gat	gtc	gag	gcg	gaa	gat	tcc	gag	taagtcgcat			1124				
Thr	Gly	Gly	Tyr	Ile	Asp	Val	Glu	Ala	Glu	Asp	Ser	Glu								
330										335										

ggtccaattc atg

1137

<210> 394

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 394

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Ala Arg Ser Arg Phe Val Ile Glu Pro Leu Glu Pro Gly Phe Gly Tyr
 20 25 30

Thr Leu Gly Asn Ser Leu Arg Arg Thr Leu Leu Ser Ser Ile Pro Gly
 35 40 45

Ala Ala Val Thr Ser Val Lys Ile Asp Gly Val Leu His Glu Phe Thr
 50 55 60

Thr Ile Ser Gly Val Lys Glu Asp Val Ser Asp Ile Ile Leu Asn Ile
 65 70 75 80

Lys Gly Leu Val Leu Ser Ser Asp Ser Asp Glu Pro Val Val Met Gln
 85 90 95

Leu Val Lys Glu Gly Pro Gly Val Val Thr Ala Gly Asp Ile Gln Pro
 100 105 110

Pro Ala Gly Val Glu Ile His Asn Pro Asp Leu His Ile Ala Thr Leu
 115 120 125

Asn Glu Thr Ala Lys Ile Glu Ile Glu Leu Ile Val Glu Arg Gly Arg
 130 135 140

Gly Tyr Val Pro Ala Thr Val Thr Ala Thr Gly Gly Glu Ile Gly Arg
 145 150 155 160

Ile Pro Val Asp Gln Ile Tyr Ser Pro Val Leu Lys Val Ser Tyr Lys
 165 170 175

Val Glu Ala Thr Arg Val Glu Gln Arg Thr Asp Phe Asp Lys Leu Val
 180 185 190

Ile Asp Val Glu Thr Lys Asn Ser Ile Thr Ala Arg Asp Ala Leu Ala
 195 200 205

Ser Ala Gly Lys Thr Leu Val Glu Leu Phe Gly Leu Ala Arg Glu Leu
 210 215 220

Asn Ile Ala Ala Glu Gly Ile Glu Ile Gly Pro Ser Pro Gln Glu Thr
 225 230 235 240

Glu Tyr Ile Ala Ala Tyr Ser Met Pro Ile Glu Asp Leu Asp Phe Ser
 245 250 255

Val Arg Ser Tyr Asn Cys Leu Lys Arg Glu Asp Ile His Thr Val Gly
 260 265 270

Glu Leu Ala Glu Arg Ala Glu Ser Asp Leu Leu Asp Ile Arg Asn Phe
 275 280 285

Gly Gln Lys Ser Ile Asn Glu Val Lys Ile Lys Leu Ala Gly Leu Gly
 290 300

Leu Thr Leu Lys Asp Ala Pro Glu Asp Phe Asp Pro Ser Thr Leu Glu
 305 310 315 320

Gly Tyr Asp Ala Glu Thr Gly Gly Tyr Ile Asp Val Glu Ala Glu Asp
 325 330 335

Ser Glu

<210> 395
 <211> 489
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(466)
 <223> RXN02981

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ggggaaaacc atcgcaacaa ccggaaaggg taactgccac atg gca cgt cta gct 115
 Met Ala Arg Leu Ala
 1 5

ggt gtt gac ctc cca cgc aac aag cgt atg gaa gtc gct ctc acc tac 163
 Gly Val Asp Leu Pro Arg Asn Lys Arg Met Glu Val Ala Leu Thr Tyr
 10 15 20

atc tac gga atc ggc cca gcc cgt tcc aag cag ctt ctc gag gag acc 211
 Ile Tyr Gly Ile Gly Pro Ala Arg Ser Lys Gln Leu Leu Glu Glu Thr
 25 30 35

gga atc tcc cca gac ctg cgc acc gac aac ctc act gat gag cag atc 259
 Gly Ile Ser Pro Asp Leu Arg Thr Asp Asn Leu Thr Asp Glu Gln Ile
 40 45 50

gct gct ctt cgt gac gtt att gaa ggc acc tgg aag gtc gag ggt gac 307
 Ala Ala Leu Arg Asp Val Ile Glu Gly Thr Trp Lys Val Glu Gly Asp
 55 60 65

ctc cgc cgc cag gta caa gct gac atc cgt cgc aag atc gaa atc ggc 355
 Leu Arg Arg Gln Val Gln Ala Asp Ile Arg Arg Lys Ile Glu Ile Gly
 70 75 80 85

tgc tac cag ggt att cgc cac cgc cgt ggc ctg cct gtt cgt ggt cag 403
 Cys Tyr Gln Gly Ile Arg His Arg Arg Gly Leu Pro Val Arg Gly Gln
 90 95 100

cgc acc aag acc aat gcg cgt act cgt aag ggt cct aag aag acg atc 451
 Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly Pro Lys Lys Thr Ile
 105 110 115

gcc gga aag aag aag taaaaatgcc tcctaaagca cgc
 Ala Gly Lys Lys Lys
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489

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<211> 122

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

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Val Ala Leu Thr Tyr Ile Tyr Gly Ile Gly Pro Ala Arg Ser Lys Gln
 20 25 30

Leu Leu Glu Glu Thr Gly Ile Ser Pro Asp Leu Arg Thr Asp Asn Leu
 35 40 45

Thr Asp Glu Gln Ile Ala Ala Leu Arg Asp Val Ile Glu Gly Thr Trp
 50 55 60

Lys Val Glu Gly Asp Leu Arg Arg Gln Val Gln Ala Asp Ile Arg Arg
 65 70 75 80

Lys Ile Glu Ile Gly Cys Tyr Gln Gly Ile Arg His Arg Arg Gly Leu
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Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly
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Pro Lys Lys Thr Ile Ala Gly Lys Lys Lys
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<211> 372

<212> DNA

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<222> (101)..(349)

<223> RXN03139

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cgggcggttcg taagtccagc tggttaaggga gtttttacca atg aag cag cgt aac 115
 Met Lys Gln Arg Asn
 1 5

aac gct aag cgc gtc cgc ctt gag cag act cgc cgc cca aag aag aac 163
 Asn Ala Lys Arg Val Arg Leu Glu Gln Thr Arg Arg Pro Lys Lys Asn
 10 15 20

ccg ctg aag gca gcg ggc atc gag aag gtg gac tac aag gac atc aac 211
 Pro Leu Lys Ala Ala Gly Ile Glu Lys Val Asp Tyr Lys Asp Ile Asn
 25 30 35

gct aac ggc aac gct tac atc aag tcc acc ttt aac aac acc atc gtt 211
Ala Asn Gly Asn Ala Tyr Ile Lys Ser Thr Phe Asn Asn Thr Ile Val
25 30 35

tcg atc act gat acc aac ggt gct gta atc tct tgg gct tcc tct ggg 259
Ser Ile Thr Asp Thr Asn Gly Ala Val Ile Ser Trp Ala Ser Ser Gly
40 45 50

cac gtc gga ttc aag ggc tca cgt aag tcc act ccg ttc gct gct cag 307
His Val Gly Phe Lys Gly Ser Arg Lys Ser Thr Pro Phe Ala Ala Gln
55 60 65

atg gct gca gag aac gct gcc cgc aag gca atg gat cac ggc atg aag 355
Met Ala Ala Glu Asn Ala Ala Arg Lys Ala Met Asp His Gly Met Lys
70 75 80 85

aag gtt gac gtt ttc gtc aag ggc cca gga tca ggc cgc gag act gca 403
Lys Val Asp Val Phe Val Lys Gly Pro Gly Ser Gly Arg Glu Thr Ala
90 95 100

atc cgt tcc ctt cag gct gca ggc ctg gag atc ggt tca atc tcc gac 451
Ile Arg Ser Leu Gln Ala Ala Gly Leu Glu Ile Gly Ser Ile Ser Asp
105 110 115

gtg acc cca cag cca cac aac ggc tgc cgt cca cca aag cgt cgt cgc 499
Val Thr Pro Gln Pro His Asn Gly Cys Arg Pro Pro Lys Arg Arg Arg
120 125 130

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Val

<210> 400

<211> 134

<212> PRT

<213> Corynebacterium glutamicum

<400> 400

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20 25 30

Asn Asn Thr Ile Val Ser Ile Thr Asp Thr Asn Gly Ala Val Ile Ser
35 40 45

Trp Ala Ser Ser Gly His Val Gly Phe Lys Gly Ser Arg Lys Ser Thr
50 55 60

Pro Phe Ala Ala Gln Met Ala Ala Glu Asn Ala Ala Arg Lys Ala Met
65 70 75 80

Asp His Gly Met Lys Lys Val Asp Val Phe Val Lys Gly Pro Gly Ser
85 90 95

Gly Arg Glu Thr Ala Ile Arg Ser Leu Gln Ala Ala Gly Leu Glu Ile
100 105 110

Gly Ser Ile Ser Asp Val Thr Pro Gln Pro His Asn Gly Cys Arg Pro

115

120

125

Pro Lys Arg Arg Arg Val
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<223> RXN00714

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accatcacat ataagacatc tcatgatcta acatttcttc atg gct acg att aca 115
Met Ala Thr Ile Thr
1 5

cgc acc gac aga ctg atc ctc gta ccg ctc act gtt gag ctc gaa gac 163
Arg Thr Asp Arg Leu Ile Leu Val Pro Leu Thr Val Glu Leu Glu Asp
10 15 20

gag gcc cac cag att tac tct gat tct cga atc tgg gaa cac cgc ccc 211
Glu Ala His Gln Ile Tyr Ser Asp Ser Arg Ile Trp Glu His Arg Pro
25 30 35

cag gcg cgt cac acc aac gtg cgt gtc acg cgc gac atc atc aag cgc 259
Gln Ala Arg His Thr Asn Val Arg Val Thr Arg Asp Ile Ile Lys Arg
40 45 50

acc aat gaa agc tgg ggc aag aaa gac ctt ggc ccc tgg ggt gtt tac 307
Thr Asn Glu Ser Trp Gly Lys Lys Asp Leu Gly Pro Trp Gly Val Tyr
55 60 65

ctc cgt gac cgc cca tcg gaa ttc gtt ggc gtt ggt ggc gtt gaa ctc 355
Leu Arg Asp Arg Pro Ser Glu Phe Val Gly Val Gly Gly Val Glu Leu
70 75 80 85

atc gac gga aaa gta tgg gac ctc aag tac cgc ctc cgc ccc gac cta 403
Ile Asp Gly Lys Val Trp Asp Leu Lys Tyr Arg Leu Arg Pro Asp Leu
90 95 100

tgg ggc aat gga tac gcc acg gaa atc tcc aac gcc gca aca ctg gcc 451
Trp Gly Asn Gly Tyr Ala Thr Glu Ile Ser Asn Ala Ala Thr Leu Ala
105 110 115

acc aag cgt atc gac gac agc ctc cca ctc acg gcc agg gtg act acc 499
Thr Lys Arg Ile Asp Asp Ser Leu Pro Leu Thr Ala Arg Val Thr Thr
120 125 130

aac cac cct gcc tca ttc cgt att ttg gaa aaa ctg gga ctc acc ccc 547
Asn His Pro Ala Ser Phe Arg Ile Leu Glu Lys Leu Gly Leu Thr Pro
135 140 145

gta tgg gaa ggc cga cga gtc gga acg gaa gat gac ccc aac gag cct 595
Val Trp Glu Gly Arg Arg Val Gly Thr Glu Asp Asp Pro Asn Glu Pro

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                                         Met Thr Pro Ser Leu
                                         1           5

ccc cgt ttc cgc agc cag aaa cct gcc gtc ggc gat cgt gtt gtt gca 163
Pro Arg Phe Arg Ser Gln Lys Pro Ala Val Gly Asp Arg Val Val Ala
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cgt cgc cgg att cct ggt gcc aat gtg cat tgg aca gat gtc att ggc 211
Arg Arg Arg Ile Pro Gly Ala Asn Val His Trp Thr Asp Val Ile Gly
                        25                      30                35

cat gtg att ggg gtg gat ccg ttg gtg gtt cgc ccg cag tcg gtt ggt 259
His Val Ile Gly Val Asp Pro Leu Val Val Arg Pro Gln Ser Val Gly
                        40                      45                50

ggg atg ccg tct gat gcg gaa gaa att gtc att cct gat gat cag ctt 307
Gly Met Pro Ser Asp Ala Glu Glu Ile Val Ile Pro Asp Asp Gln Leu
                        55                      60                65

gag gtg att aag att ttg tcg ccg cgc acc att agg aat tcg gat att 355
Glu Val Ile Lys Ile Leu Ser Pro Arg Thr Ile Arg Asn Ser Asp Ile
                        70                      75                80                85

cgt gcg gtg gag gtt gcc acg gcg aag gcc ttt ccg ggg ctg gtc aat 403
Arg Ala Val Glu Val Ala Thr Ala Lys Ala Phe Pro Gly Leu Val Asn
                        90                      95                100

gag tgg cat gat ggt tgg ctg ctg cgt gcc ggt gat ggc att gcg gag 451
Glu Trp His Asp Gly Trp Leu Leu Arg Ala Gly Asp Gly Ile Ala Glu
                        105                      110                115

cgt tct aat tct gcg tcg cca ctc ggc cca agt gtc ggt tct gag ccg 499
Arg Ser Asn Ser Ala Ser Pro Leu Gly Pro Ser Val Gly Ser Glu Pro
                        120                      125                130

gta ccg atg gag gat att tcg cgg ttt tat gca cgt cac gat ctc ccc 547
Val Pro Met Glu Asp Ile Ser Arg Phe Tyr Ala Arg His Asp Leu Pro
                        135                      140                145

gtg aag ctg cac att ccg gag cgg att ggt cgg cct gcg cag aaa gtc 595
Val Lys Leu His Ile Pro Glu Arg Ile Gly Arg Pro Ala Gln Lys Val
                        150                      155                160                165

att gac gcc gat ccc cag aaa tgg gtg atg ggc ccg gag att ttg gtg 643
Ile Asp Ala Asp Pro Gln Lys Trp Val Met Gly Pro Glu Ile Leu Val
                        170                      175                180

atg acg aaa tct ttg gac cat gtg gag tcg cac gaa ttg ccc ggt ggc 691
Met Thr Lys Ser Leu Asp His Val Glu Ser His Glu Leu Pro Gly Gly
                        185                      190                195

cta gaa ttt agc gtc gat aag cag cct gac cag gag tgg ctg ggc atg 739
Leu Glu Phe Ser Val Asp Lys Gln Pro Asp Gln Glu Trp Leu Gly Met
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 215 220 225
 cgc acg caa atc gag ggc cgc atg ggg ttc ggg cgc ctg acc acg ccg 835
 Arg Thr Gln Ile Glu Gly Arg Met Gly Phe Gly Arg Leu Thr Thr Pro
 230 235 240 245
 gcg ggg caa acc gtc gcg atc acg cgc gcc acc atc acg gct gcg gag 883
 Ala Gly Gln Thr Val Ala Ile Thr Arg Ala Thr Ile Thr Ala Ala Glu
 250 255 260
 gag cgc ata ttt ttg ggc tat tca gcg gtc gag gtg gat cct gct ttt 931
 Glu Arg Ile Phe Leu Gly Tyr Ser Ala Val Glu Val Asp Pro Ala Phe
 265 270 275
 cga cgt cag ggg ctg ggc acc gcg ctc ggc tcg cgc atc cag gag tgg 979
 Arg Arg Gln Gly Leu Gly Thr Ala Leu Gly Ser Arg Ile Gln Glu Trp
 280 285 290
 ggc gcc gag caa cac gca cag gag gca tat ctc cag gtt gtc gcc cat 1027
 Gly Ala Glu Gln His Ala Gln Glu Ala Tyr Leu Gln Val Val Ala His
 295 300 305
 aat gaa gca ggt atc ggc ctg tat caa aag ctc ggg ttc agt gaa cac 1075
 Asn Glu Ala Gly Ile Gly Leu Tyr Gln Lys Leu Gly Phe Ser Glu His
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gta 1128

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 <213> Corynebacterium glutamicum

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 20 25 30
 Thr Asp Val Ile Gly His Val Ile Gly Val Asp Pro Leu Val Val Arg
 35 40 45
 Pro Gln Ser Val Gly Gly Met Pro Ser Asp Ala Glu Glu Ile Val Ile
 50 55 60
 Pro Asp Asp Gln Leu Glu Val Ile Lys Ile Leu Ser Pro Arg Thr Ile
 65 70 75 80
 Arg Asn Ser Asp Ile Arg Ala Val Glu Val Ala Thr Ala Lys Ala Phe
 85 90 95
 Pro Gly Leu Val Asn Glu Trp His Asp Gly Trp Leu Leu Arg Ala Gly

100	105	110
Asp Gly Ile Ala Glu Arg Ser Asn Ser Ala Ser Pro Leu Gly Pro Ser 115 120 125		
Val Gly Ser Glu Pro Val Pro Met Glu Asp Ile Ser Arg Phe Tyr Ala 130 135 140		
Arg His Asp Leu Pro Val Lys Leu His Ile Pro Glu Arg Ile Gly Arg 145 150 155 160		
Pro Ala Gln Lys Val Ile Asp Ala Asp Pro Gln Lys Trp Val Met Gly 165 170 175		
Pro Glu Ile Leu Val Met Thr Lys Ser Leu Asp His Val Glu Ser His 180 185 190		
Glu Leu Pro Gly Gly Leu Glu Phe Ser Val Asp Lys Gln Pro Asp Gln 195 200 205		
Glu Trp Leu Gly Met Tyr His Phe Arg Gly Gln Ala Leu Pro Ala His 210 215 220		
Ala Leu Glu Leu Leu Arg Thr Gln Ile Glu Gly Arg Met Gly Phe Gly 225 230 235 240		
Arg Leu Thr Thr Pro Ala Gly Gln Thr Val Ala Ile Thr Arg Ala Thr 245 250 255		
Ile Thr Ala Ala Glu Glu Arg Ile Phe Leu Gly Tyr Ser Ala Val Glu 260 265 270		
Val Asp Pro Ala Phe Arg Arg Gln Gly Leu Gly Thr Ala Leu Gly Ser 275 280 285		
Arg Ile Gln Glu Trp Gly Ala Glu Gln His Ala Gln Glu Ala Tyr Leu 290 295 300		
Gln Val Val Ala His Asn Glu Ala Gly Ile Gly Leu Tyr Gln Lys Leu 305 310 315 320		
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Leu Asp Glu Gly Asn

1

5

acc gtt ccg ttc atc gcc agg tac cgc aag gaa atc act ggg gga ctc	163
Thr Val Pro Phe Ile Ala Arg Tyr Arg Lys Glu Ile Thr Gly Gly Leu	
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gat gat acc caa ctg cgt gac ctg gaa gaa cgc ctc agt tac ctc cgt	211
Asp Asp Thr Gln Leu Arg Asp Leu Glu Glu Arg Leu Ser Tyr Leu Arg	
25 30 35	
gag ctg gag gat cgt aaa caa agc atc ctc gcc gcg att gag gaa caa	259
Glu Leu Glu Asp Arg Lys Gln Ser Ile Leu Ala Ala Ile Glu Glu Gln	
40 45 50	
ggc aaa ctc acc gac gat tta cgc tcg ctg att ttg gga tgc gac acc	307
Gly Lys Leu Thr Asp Asp Leu Arg Ser Leu Ile Leu Gly Cys Asp Thr	
55 60 65	
aag gct cgc ctg gag gat ctg tac ctg ccg ttc aaa aaa cgg cgc aag	355
Lys Ala Arg Leu Glu Asp Leu Tyr Leu Pro Phe Lys Lys Arg Arg Lys	
70 75 80 85	
acg aag gcc gat atc gct agg gag gcg ggc ctg gag ggg ctc gtc gat	403
Thr Lys Ala Asp Ile Ala Arg Glu Ala Gly Leu Glu Gly Leu Val Asp	
90 95 100	
aag ctt atc gac gcc ccg tcc ctc gac gcc gca gcg cag gca gct gca	451
Lys Leu Ile Asp Ala Pro Ser Leu Asp Ala Ala Ala Gln Ala Ala Ala	
105 110 115	
ttt acg act gag ggc ttt gag gat tcc aaa aaa gtt ttg gat ggc gct	499
Phe Thr Thr Glu Gly Phe Glu Asp Ser Lys Lys Val Leu Asp Gly Ala	
120 125 130	
cgc gcc att ttg att gac cgc ttc gcg ctc gat gcc gat ttg gtg ggc	547
Arg Ala Ile Leu Ile Asp Arg Phe Ala Leu Asp Ala Asp Leu Val Gly	
135 140 145	
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Glu Val Arg Glu Gln Met Tyr Arg Ala Gly Ser Met Ala Ala Ser Val	
150 155 160 165	
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Val Ala Gly Lys Glu Gln Glu Gly Ala Lys Phe Lys Asp Tyr Phe Glu	
170 175 180	
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Phe Ser Glu Pro Phe Asp Lys Leu Pro Ser His Arg Ile Leu Ala Leu	
185 190 195	
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Leu Arg Gly Glu Asn Glu Gly Val Leu Ser Leu Asn Leu Asp Ala Gly	
200 205 210	
gac gac ata atc tac gaa ggt ttg atc gcc gac cga ttc tcc ctg gac	787
Asp Asp Ile Ile Tyr Glu Gly Leu Ile Ala Asp Arg Phe Ser Leu Asp	
215 220 225	
acc cac act tct agc tgg ctg gct gag gct gtg cgc tgg ggt tgg cgc	835
Thr His Thr Ser Ser Trp Leu Ala Glu Ala Val Arg Trp Gly Trp Arg	
230 235 240 245	

acc aaa ctg tat gtg tcc tcc gga ttg gat gtg cgc atg cgt ctg aaa	883
Thr Lys Leu Tyr Val Ser Ser Gly Leu Asp Val Arg Met Arg Leu Lys	
250 255 260	
gaa aaa gca gag gaa ggc gca ctc gat gtg ttt gcc acc aac ctc cgc	931
Glu Lys Ala Glu Glu Gly Ala Leu Asp Val Phe Ala Thr Asn Leu Arg	
265 270 275	
gac gtt ctc ctt gca gct ccc gct ggt cag cgc tcc aca att ggc ctt	979
Asp Val Leu Leu Ala Ala Pro Ala Gly Gln Arg Ser Thr Ile Gly Leu	
280 285 290	
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Asp Pro Gly Phe Arg Asn Gly Val Lys Val Ala Val Val Asp Ser Thr	
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Gly Lys Asp Val Ala Thr Ile Val Tyr Pro His Gln Pro Gln Asn	
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Arg Trp Lys Glu Ala Val Ser Glu Leu Ala Asn Leu Cys Ala Thr His	
330 335 340	
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Gly Val Glu Leu Met Ala Ile Gly Asn Gly Thr Ala Ser Arg Glu Thr	
345 350 355	
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Glu Lys Leu Ala Gly Glu Val Ala Asp Met Ile Lys Ala Ala Gly Gly	
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Thr Arg Pro Thr Pro Val Val Val Ser Glu Ser Gly Ala Ser Val Tyr	
375 380 385	
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Ser Ala Ser Pro Ile Ala Ala Glu Glu Phe Pro Asp Met Asp Val Ser	
390 395 400 405	
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Leu Arg Gly Ala Val Ser Ile Ala Arg Arg Leu Gln Asp Pro Leu Ala	
410 415 420	
gag ctc gtc aag att gag ccc aaa gcc atc gga gtc ggc cag tac caa	1411
Glu Leu Val Lys Ile Glu Pro Lys Ala Ile Gly Val Gly Gln Tyr Gln	
425 430 435	
cac gat gtc aac cag gtt gca ctt gcc aaa acc ctt gat ggt gtc gtc	1459
His Asp Val Asn Gln Val Ala Leu Ala Lys Thr Leu Asp Gly Val Val	
440 445 450	
gaa gac gca gta aac gca gtc gga gtt aac ctc aac acc gca tcc gca	1507
Glu Asp Ala Val Asn Ala Val Gly Val Asn Leu Asn Thr Ala Ser Ala	
455 460 465	
cca ctt ctt acc cga gtt gcc gga gtg acc tcc acc ttg gca aac aat	1555
Pro Leu Leu Thr Arg Val Ala Gly Val Thr Ser Thr Leu Ala Asn Asn	
470 475 480 485	
atc gtg gcc tac cgc aac gaa aac ggt gga ttc tcc tcc cga aaa gaa	1603

Ile Val Ala Tyr Arg Asn Glu Asn Gly Gly Phe Ser Ser Arg Lys Glu	
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Leu Asn Lys Val Pro Arg Leu Gly Pro Lys Ala Phe Glu Gln Cys Ala	
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ggc ttc ctc cgc att tct gga tcc acc gac cct ctc gac gcc tcc gct	1699
Gly Phe Leu Arg Ile Ser Gly Ser Thr Asp Pro Leu Asp Ala Ser Ala	
520	525 530
gtt cac ccc gag gcg tac cca gtt gtt cgc aac att gcg aaa gcc aca	1747
Val His Pro Glu Ala Tyr Pro Val Val Arg Asn Ile Ala Lys Ala Thr	
535	540 545
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Gly Leu Asp Val Ser Gly Leu Ile Gly Asn Ser Ala Val Leu Thr Lys	
550	555 560 565
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Leu Lys Pro Ala Asp Phe Ala Asp Glu Arg Phe Gly Ile Pro Thr Val	
570	575 580
acc gac atc atc gcc gag ctg gat aaa ccc gga cgt gac ccc cgc cca	1891
Thr Asp Ile Ile Ala Glu Leu Asp Lys Pro Gly Arg Asp Pro Arg Pro	
585	590 595
gaa ttc aaa acc gcc agc ttc aaa gaa ggc gtg gag aaa atc tcc gac	1939
Glu Phe Lys Thr Ala Ser Phe Lys Glu Gly Val Glu Lys Ile Ser Asp	
600	605 610
ctc aca ccc ggc atg atc ctg gaa gga act gtc acc aac gtt gcg gcg	1987
Leu Thr Pro Gly Met Ile Leu Glu Gly Thr Val Thr Asn Val Ala Ala	
615	620 625
ttc ggc gca ttc gtt gac gtg gga gtg cac cga gat ggc ctc gtt cac	2035
Phe Gly Ala Phe Val Asp Val Gly Val His Arg Asp Gly Leu Val His	
630	635 640 645
gtt tcc gcg atg agc gac aaa ttc atc tcc aac ccc cac gaa gtt gtt	2083
Val Ser Ala Met Ser Asp Lys Phe Ile Ser Asn Pro His Glu Val Val	
650	655 660
cgc tct ggt gag gtc gtg aag gta aag gtc atg gaa gtt gac gtc gac	2131
Arg Ser Gly Glu Val Val Lys Val Lys Val Met Glu Val Asp Val Asp	
665	670 675
cgc aaa cgc atc ggc ctt tcc ctc cgc ttg acc gat gaa ccc ggt gcc	2179
Arg Lys Arg Ile Gly Leu Ser Leu Arg Leu Thr Asp Glu Pro Gly Ala	
680	685 690
cca gct ccg caa aag cgc gga aac cga cca gcc aaa cag cag cga gct	2227
Pro Ala Pro Gln Lys Arg Gly Asn Arg Pro Ala Lys Gln Gln Arg Ala	
695	700 705
ccg caa aaa cag tcc gct aag ccc gcc aca ggt tcc atg gca gat gct	2275
Pro Gln Lys Gln Ser Ala Lys Pro Ala Thr Gly Ser Met Ala Asp Ala	
710	715 720 725
tta cga cgc gcc ggc ctc ggt ggc taaggcaact ttcaaacc aa gcg	2322
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730

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<400> 406

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20 25 30

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35 40 45

Ala Ile Glu Glu Gln Gly Lys Leu Thr Asp Asp Leu Arg Ser Leu Ile
50 55 60

Leu Gly Cys Asp Thr Lys Ala Arg Leu Glu Asp Leu Tyr Leu Pro Phe
65 70 75 80

Lys Lys Arg Arg Lys Thr Lys Ala Asp Ile Ala Arg Glu Ala Gly Leu
85 90 95

Glu Gly Leu Val Asp Lys Leu Ile Asp Ala Pro Ser Leu Asp Ala Ala
100 105 110

Ala Gln Ala Ala Ala Phe Thr Thr Glu Gly Phe Glu Asp Ser Lys Lys
115 120 125

Val Leu Asp Gly Ala Arg Ala Ile Leu Ile Asp Arg Phe Ala Leu Asp
130 135 140

Ala Asp Leu Val Gly Glu Val Arg Glu Gln Met Tyr Arg Ala Gly Ser
145 150 155 160

Met Ala Ala Ser Val Val Ala Gly Lys Glu Gln Glu Gly Ala Lys Phe
165 170 175

Lys Asp Tyr Phe Glu Phe Ser Glu Pro Phe Asp Lys Leu Pro Ser His
180 185 190

Arg Ile Leu Ala Leu Leu Arg Gly Glu Asn Glu Gly Val Leu Ser Leu
195 200 205

Asn Leu Asp Ala Gly Asp Asp Ile Ile Tyr Glu Gly Leu Ile Ala Asp
210 215 220

Arg Phe Ser Leu Asp Thr His Thr Ser Ser Trp Leu Ala Glu Ala Val
225 230 235 240

Arg Trp Gly Trp Arg Thr Lys Leu Tyr Val Ser Ser Gly Leu Asp Val
245 250 255

Arg Met Arg Leu Lys Glu Lys Ala Glu Glu Gly Ala Leu Asp Val Phe
260 265 270

Ala Thr Asn Leu Arg Asp Val Leu Leu Ala Ala Pro Ala Gly Gln Arg

275					280					285					
Ser	Thr	Ile	Gly	Leu	Asp	Pro	Gly	Phe	Arg	Asn	Gly	Val	Lys	Val	Ala
290						295					300				
Val	Val	Asp	Ser	Thr	Gly	Lys	Asp	Val	Ala	Thr	Thr	Ile	Val	Tyr	Pro
305					310					315					320
His	Gln	Pro	Gln	Asn	Arg	Trp	Lys	Glu	Ala	Val	Ser	Glu	Leu	Ala	Asn
				325					330					335	
Leu	Cys	Ala	Thr	His	Gly	Val	Glu	Leu	Met	Ala	Ile	Gly	Asn	Gly	Thr
			340					345					350		
Ala	Ser	Arg	Glu	Thr	Glu	Lys	Leu	Ala	Gly	Glu	Val	Ala	Asp	Met	Ile
		355					360					365			
Lys	Ala	Ala	Gly	Gly	Thr	Arg	Pro	Thr	Pro	Val	Val	Val	Ser	Glu	Ser
						375					380				
Gly	Ala	Ser	Val	Tyr	Ser	Ala	Ser	Pro	Ile	Ala	Ala	Glu	Glu	Phe	Pro
385						390					395				400
Asp	Met	Asp	Val	Ser	Leu	Arg	Gly	Ala	Val	Ser	Ile	Ala	Arg	Arg	Leu
				405					410					415	
Gln	Asp	Pro	Leu	Ala	Glu	Leu	Val	Lys	Ile	Glu	Pro	Lys	Ala	Ile	Gly
			420					425						430	
Val	Gly	Gln	Tyr	Gln	His	Asp	Val	Asn	Gln	Val	Ala	Leu	Ala	Lys	Thr
			435				440					445			
Leu	Asp	Gly	Val	Val	Glu	Asp	Ala	Val	Asn	Ala	Val	Gly	Val	Asn	Leu
			450			455					460				
Asn	Thr	Ala	Ser	Ala	Pro	Leu	Leu	Thr	Arg	Val	Ala	Gly	Val	Thr	Ser
465						470					475				480
Thr	Leu	Ala	Asn	Asn	Ile	Val	Ala	Tyr	Arg	Asn	Glu	Asn	Gly	Gly	Phe
				485					490					495	
Ser	Ser	Arg	Lys	Glu	Leu	Asn	Lys	Val	Pro	Arg	Leu	Gly	Pro	Lys	Ala
			500					505					510		
Phe	Glu	Gln	Cys	Ala	Gly	Phe	Leu	Arg	Ile	Ser	Gly	Ser	Thr	Asp	Pro
			515				520					525			
Leu	Asp	Ala	Ser	Ala	Val	His	Pro	Glu	Ala	Tyr	Pro	Val	Val	Arg	Asn
			530			535					540				
Ile	Ala	Lys	Ala	Thr	Gly	Leu	Asp	Val	Ser	Gly	Leu	Ile	Gly	Asn	Ser
545						550					555				560
Ala	Val	Leu	Thr	Lys	Leu	Lys	Pro	Ala	Asp	Phe	Ala	Asp	Glu	Arg	Phe
				565					570					575	
Gly	Ile	Pro	Thr	Val	Thr	Asp	Ile	Ile	Ala	Glu	Leu	Asp	Lys	Pro	Gly
			580					585					590		
Arg	Asp	Pro	Arg	Pro	Glu	Phe	Lys	Thr	Ala	Ser	Phe	Lys	Glu	Gly	Val
			595				600					605			

Glu Lys Ile Ser Asp Leu Thr Pro Gly Met Ile Leu Glu Gly Thr Val
 610 615 620
 Thr Asn Val Ala Ala Phe Gly Ala Phe Val Asp Val Gly Val His Arg
 625 630 635 640
 Asp Gly Leu Val His Val Ser Ala Met Ser Asp Lys Phe Ile Ser Asn
 645 650 655
 Pro His Glu Val Val Arg Ser Gly Glu Val Val Lys Val Lys Val Met
 660 665 670
 Glu Val Asp Val Asp Arg Lys Arg Ile Gly Leu Ser Leu Arg Leu Thr
 675 680 685
 Asp Glu Pro Gly Ala Pro Ala Pro Gln Lys Arg Gly Asn Arg Pro Ala
 690 695 700
 Lys Gln Gln Arg Ala Pro Gln Lys Gln Ser Ala Lys Pro Ala Thr Gly
 705 710 715 720
 Ser Met Ala Asp Ala Leu Arg Arg Ala Gly Leu Gly Gly
 725 730

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<211> 1286

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1263)

<223> RXA00157

<400> 407

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gtc cag acc gag gct gca att gcc gca aac agc gag cag ctc aat gtc	96
Val Gln Thr Glu Ala Ala Ile Ala Asn Ser Glu Gln Leu Asn Val	
20 25 30	
ttg act acc aat cgc agt acc ttg gtt gcc cag cgt gat ggg gct gag	144
Leu Thr Thr Asn Arg Ser Thr Leu Val Ala Gln Arg Asp Gly Ala Glu	
35 40 45	
cgc aac ttg gcc atc gct cgt gcg cag gcg gat aat ctg caa ggt cag	192
Arg Asn Leu Ala Ile Ala Arg Ala Gln Ala Asp Asn Leu Gln Gly Gln	
50 55 60	
cgt gct gag tac gag gaa ttc cag cag gca gag cag gct cgc atc cag	240
Arg Ala Glu Tyr Glu Glu Phe Gln Gln Ala Glu Gln Ala Arg Ile Gln	
65 70 75 80	
gcg gaa gcg gaa gct cag gct gct gcg gag gag aag cgt cgt gcc gat	288
Ala Glu Ala Glu Ala Gln Ala Ala Ala Glu Glu Lys Arg Arg Ala Asp	
85 90 95	

gag gct gct gca cag gca gcc gct gaa gct caa gaa gct gcc cag caa	336
Glu Ala Ala Ala Gln Ala Ala Ala Glu Ala Gln Glu Ala Ala Gln Gln	
100 105 110	
gct cag gcg gcg gag gaa gcc caa gcc gcg caa gca gct gag aca gca	384
Ala Gln Ala Ala Glu Glu Ala Gln Ala Ala Gln Ala Ala Glu Thr Ala	
115 120 125	
caa gcc caa gcc gcg caa gct gcg gaa acc caa gct gca caa gcc gcg	432
Gln Ala Gln Ala Ala Gln Ala Ala Glu Thr Gln Ala Ala Gln Ala Ala	
130 135 140	
caa gct cag gca gaa gcg aat gat cgt gcc gcc gcg caa cag cgt gct	480
Gln Ala Gln Ala Glu Ala Asn Asp Arg Ala Ala Ala Gln Gln Arg Ala	
145 150 155 160	
gca gag gct caa gca gca gcg gaa cag gcg caa cgt gag gct gac gct	528
Ala Glu Ala Gln Ala Ala Ala Glu Gln Ala Gln Arg Glu Ala Asp Ala	
165 170 175	
cag gcg gcc aac gat gcc caa gct cag gca ctg cgt gaa cag gcg ctc	576
Gln Ala Ala Asn Asp Ala Gln Ala Gln Ala Leu Arg Glu Gln Ala Leu	
180 185 190	
acc gca gcc tcc atc gct gcg gct gct cta att gcg gcg agc cag tcc	624
Thr Ala Ala Ser Ile Ala Ala Ala Leu Ile Ala Ala Ser Gln Ser	
195 200 205	
agc cat gcc act act caa aat cct tac cca act gat gaa gac gcg gat	672
Ser His Ala Thr Thr Gln Asn Pro Tyr Pro Thr Asp Glu Asp Ala Asp	
210 215 220	
ccg acc gat att gcg gac atc caa ggc cca acg cag cca ggt acg ggt	720
Pro Thr Asp Ile Ala Asp Ile Gln Gly Pro Thr Gln Pro Gly Thr Gly	
225 230 235 240	
gag tct gga gat tcc cag agc aac tcc agc gac aac gat tcc aca ggc	768
Glu Ser Gly Asp Ser Gln Ser Asn Ser Ser Asp Asn Asp Ser Thr Gly	
245 250 255	
aac gat tcc aca ggc tct gac tct tca gat tca gat tcc tcc ggc aac	816
Asn Asp Ser Thr Gly Ser Asp Ser Ser Asp Ser Asp Ser Ser Gly Asn	
260 265 270	
gat tct tca gag gtt att tcc ggc gat cgt tcc gct cag att gag act	864
Asp Ser Ser Glu Val Ile Ser Gly Asp Arg Ser Ala Gln Ile Glu Thr	
275 280 285	
gtg att gcg cgc gcc atg agc cag ttg ggt gtg cag tac gca tgg ggt	912
Val Ile Ala Arg Ala Met Ser Gln Leu Gly Val Gln Tyr Ala Trp Gly	
290 295 300	
ggc ggt aac gct aat ggc cca act ctg ggt atc cgt gac ggt ggc gtg	960
Gly Gly Asn Ala Asn Gly Pro Thr Leu Gly Ile Arg Asp Gly Gly Val	
305 310 315 320	
gcg gac tct tac ggc gat tac aac aag gtt ggc ttc gac tgc tct gga	1008
Ala Asp Ser Tyr Gly Asp Tyr Asn Lys Val Gly Phe Asp Cys Ser Gly	
325 330 335	
ctg acc ttg tat gcg ttt gcg ggt gtg gga att tca ctt cct cac tac	1056

Leu Thr Leu Tyr Ala Phe Ala Gly Val Gly Ile Ser Leu Pro His Tyr
 340 345 350
 acg ggc tac cag tac cag cac ggc acc aag gtg tcg cct tct gag atg 1104
 Thr Gly Tyr Gln Tyr Gln His Gly Thr Lys Val Ser Pro Ser Glu Met
 355 360 365
 caa cgt ggc gat ctg atc ttc tat ggt ccg gga gcg tct cag cac gtg 1152
 Gln Arg Gly Asp Leu Ile Phe Tyr Gly Pro Gly Ala Ser Gln His Val
 370 375 380
 gca att tac ctc ggt gat ggt cag atg att gag gct ccg aat tcg ggt 1200
 Ala Ile Tyr Leu Gly Asp Gly Gln Met Ile Glu Ala Pro Asn Ser Gly
 385 390 395 400
 tct gtc gtg aag att tct cct gtt cgc tgg agc gga atg acc gag agc 1248
 Ser Val Val Lys Ile Ser Pro Val Arg Trp Ser Gly Met Thr Glu Ser
 405 410 415
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 Val Val Arg Leu Ile
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 20 25 30
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 35 40 45
 Arg Asn Leu Ala Ile Ala Arg Ala Gln Ala Asp Asn Leu Gln Gly Gln
 50 55 60
 Arg Ala Glu Tyr Glu Glu Phe Gln Gln Ala Glu Gln Ala Arg Ile Gln
 65 70 75 80
 Ala Glu Ala Glu Ala Gln Ala Ala Ala Glu Glu Lys Arg Arg Ala Asp
 85 90 95
 Glu Ala Ala Ala Gln Ala Ala Ala Glu Ala Gln Glu Ala Ala Gln Gln
 100 105 110
 Ala Gln Ala Ala Glu Glu Ala Gln Ala Ala Gln Ala Ala Glu Thr Ala
 115 120 125
 Gln Ala Gln Ala Ala Gln Ala Ala Glu Thr Gln Ala Ala Gln Ala Ala
 130 135 140
 Gln Ala Gln Ala Glu Ala Asn Asp Arg Ala Ala Ala Gln Gln Arg Ala
 145 150 155 160
 Ala Glu Ala Gln Ala Ala Ala Glu Gln Ala Gln Arg Glu Ala Asp Ala

165					170					175					
Gln	Ala	Ala	Asn	Asp	Ala	Gln	Ala	Gln	Ala	Leu	Arg	Glu	Gln	Ala	Leu
			180					185					190		
Thr	Ala	Ala	Ser	Ile	Ala	Ala	Ala	Ala	Leu	Ile	Ala	Ala	Ser	Gln	Ser
			195				200					205			
Ser	His	Ala	Thr	Thr	Gln	Asn	Pro	Tyr	Pro	Thr	Asp	Glu	Asp	Ala	Asp
	210					215					220				
Pro	Thr	Asp	Ile	Ala	Asp	Ile	Gln	Gly	Pro	Thr	Gln	Pro	Gly	Thr	Gly
225					230					235					240
Glu	Ser	Gly	Asp	Ser	Gln	Ser	Asn	Ser	Ser	Asp	Asn	Asp	Ser	Thr	Gly
				245					250					255	
Asn	Asp	Ser	Thr	Gly	Ser	Asp	Ser	Ser	Asp	Ser	Asp	Ser	Ser	Gly	Asn
			260					265						270	
Asp	Ser	Ser	Glu	Val	Ile	Ser	Gly	Asp	Arg	Ser	Ala	Gln	Ile	Glu	Thr
			275				280					285			
Val	Ile	Ala	Arg	Ala	Met	Ser	Gln	Leu	Gly	Val	Gln	Tyr	Ala	Trp	Gly
	290					295					300				
Gly	Gly	Asn	Ala	Asn	Gly	Pro	Thr	Leu	Gly	Ile	Arg	Asp	Gly	Gly	Val
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Ala	Asp	Ser	Tyr	Gly	Asp	Tyr	Asn	Lys	Val	Gly	Phe	Asp	Cys	Ser	Gly
				325					330					335	
Leu	Thr	Leu	Tyr	Ala	Phe	Ala	Gly	Val	Gly	Ile	Ser	Leu	Pro	His	Tyr
			340					345					350		
Thr	Gly	Tyr	Gln	Tyr	Gln	His	Gly	Thr	Lys	Val	Ser	Pro	Ser	Glu	Met
		355					360					365			
Gln	Arg	Gly	Asp	Leu	Ile	Phe	Tyr	Gly	Pro	Gly	Ala	Ser	Gln	His	Val
	370					375					380				
Ala	Ile	Tyr	Leu	Gly	Asp	Gly	Gln	Met	Ile	Glu	Ala	Pro	Asn	Ser	Gly
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Ser	Val	Val	Lys	Ile	Ser	Pro	Val	Arg	Trp	Ser	Gly	Met	Thr	Glu	Ser
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<211> 972

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(949)

<223> RXA00208

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Pro Arg Lys Arg Arg Glu Met Lys Ile Lys Thr Ala Thr Val Thr Gly
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gtg	cgt	caa	att	tcc	ccc	gat	ctc	atc	cgc	ttc	agc	ttc	gac	tgc	cca	211
Val	Arg	Gln	Ile	Ser	Pro	Asp	Leu	Ile	Arg	Phe	Ser	Phe	Asp	Cys	Pro	
			25					30					35			

gaa atc gtt ggc gcc gac ctg ggg ttc acg gac cat tac atc aag atc 259
Glu Ile Val Gly Ala Asp Leu Gly Phe Thr Asp His Tyr Ile Lys Ile
40 45 50

ctc ttc gtg cca gca ggt gcg gat tac tcc tgg cct ttc gac atg gca 307
Leu Phe Val Pro Ala Gly Ala Asp Tyr Ser Trp Pro Phe Asp Met Ala
55 60 65

gaa att gcg gaa acc cag ccc cgt gag ctg caa cca gtg cgc cgc acc 355
Glu Ile Ala Glu Thr Gln Pro Arg Glu Leu Gln Pro Val Arg Arg Thr
70 75 80 85

tac	act	ttc	cgc	acg	gtt	gac	act	gtc	gca	ggc	aca	ttt	gac	ata	gat	403
Tyr	Thr	Phe	Arg	Thr	Val	Asp	Thr	Val	Ala	Gly	Thr	Phe	Asp	Ile	Asp	
				90					95					100		

ttc gtt gcg cac ggc acc gat ggc ctt gcc ggt cct tgg gcg cag cag 451
 Phe Val Ala His Gly Thr Asp Gly Leu Ala Gly Pro Trp Ala Gln Gln
 105 110 115

gca cag gta ggt gat gtc atc gcg ttc ggc ggc cca ggt ggc gca tgg 499
Ala Gln Val Gly Asp Val Ile Ala Phe Gly Gly Pro Gly Gly Ala Trp
120 125 130

aag cca gaa acc acc tat gag cac tac gtt ctc gca ggc gat gaa gcc 547
Lys Pro Glu Thr Thr Tyr Glu His Tyr Val Leu Ala Gly Asp Glu Ala
135 140 145

gca gca ccc gca att ttc gca gcc tta gaa cac cta ccc gcc ggc acc 595
Ala Ala Pro Ala Ile Phe Ala Ala Leu Glu His Leu Pro Ala Gly Thr
150 155 160 165

acc gcc aaa gcc ttc att gaa atc tcc tcc aac gaa gcg cgt ttc aac 643
Thr Ala Lys Ala Phe Ile Glu Ile Ser Ser Asn Glu Ala Arg Phe Asn
170 175 180

gcc cca gcc agc gac aac atc gag gtt gtc tgg gtg ccc cgc gac ggc 691
Ala Pro Ala Ser Asp Asn Ile Glu Val Val Trp Val Pro Arg Asp Gly
185 190 195

gcc acc cac ggt aca ttg ctt atc gac gcc ctc cgc cag gac ggc tac 739
Ala Thr His Gly Thr Leu Leu Ile Asp Ala Leu Arg Gln Asp Gly Tyr
200 205 210

cca acc aag aaa act tcc tgg ttc atc cac gga gtc gcc gaa atg gtg 787
Pro Thr Lys Lys Thr Ser Trp Phe Ile His Gly Val Ala Glu Met Val

215	220	225	
aag gaa acc cgc aaa ttc ctc ttc gtg gaa ggc aac gta gac aaa gct			835
Lys Glu Thr Arg Lys Phe Leu Phe Val Glu Gly Asn Val Asp Lys Ala			
230	235	240	245
gat gca tcc att tcc gga tac tgg cgc ctt ggc atg acc gaa gac cag			883
Asp Ala Ser Ile Ser Gly Tyr Trp Arg Leu Gly Met Thr Glu Asp Gln			
250	255		260
tgg cag gcc tcc aag cgg gag ttc aat gag caa aat gag gca gaa gaa			931
Trp Gln Ala Ser Lys Arg Glu Phe Asn Glu Gln Asn Glu Ala Glu Glu			
265	270		275
ctc gcg ctc agc aag gca taagggcaag gggttctaga aag			972
Leu Ala Leu Ser Lys Ala			
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<211> 283

<212> PRT

<213> Corynebacterium glutamicum

<400> 410

Met Asn Thr Pro Ala Pro Arg Lys Arg Arg Glu Met Lys Ile Lys Thr
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20 25 30

Ser Phe Asp Cys Pro Glu Ile Val Gly Ala Asp Leu Gly Phe Thr Asp
35 40 45

His Tyr Ile Lys Ile Leu Phe Val Pro Ala Gly Ala Asp Tyr Ser Trp
50 55 60

Pro Phe Asp Met Ala Glu Ile Ala Glu Thr Gln Pro Arg Glu Leu Gln
65 70 75 80

Pro Val Arg Arg Thr Tyr Thr Phe Arg Thr Val Asp Thr Val Ala Gly
85 90 95

Thr Phe Asp Ile Asp Phe Val Ala His Gly Thr Asp Gly Leu Ala Gly
100 105 110

Pro Trp Ala Gln Gln Ala Gln Val Gly Asp Val Ile Ala Phe Gly Gly
115 120 125

Pro Gly Gly Ala Trp Lys Pro Glu Thr Thr Tyr Glu His Tyr Val Leu
130 135 140

Ala Gly Asp Glu Ala Ala Ala Pro Ala Ile Phe Ala Ala Leu Glu His
145 150 155 160

Leu Pro Ala Gly Thr Thr Ala Lys Ala Phe Ile Glu Ile Ser Ser Asn
165 170 175

Glu Ala Arg Phe Asn Ala Pro Ala Ser Asp Asn Ile Glu Val Val Trp
180 185 190

Val Pro Arg Asp Gly Ala Thr His Gly Thr Leu Leu Ile Asp Ala Leu
 195 200 205

Arg Gln Asp Gly Tyr Pro Thr Lys Lys Thr Ser Trp Phe Ile His Gly
 210 215 220

Val Ala Glu Met Val Lys Glu Thr Arg Lys Phe Leu Phe Val Glu Gly
 225 230 235 240

Asn Val Asp Lys Ala Asp Ala Ser Ile Ser Gly Tyr Trp Arg Leu Gly
 245 250 255

Met Thr Glu Asp Gln Trp Gln Ala Ser Lys Arg Glu Phe Asn Glu Gln
 260 265 270

Asn Glu Ala Glu Glu Leu Ala Leu Ser Lys Ala
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<212> DNA

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<220>

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<222> (26)..(388)

<223> RXA00967

<400> 411

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 Asn Asn Asn Asp Arg Pro Val Met Pro Gly Glu Ile Leu Arg Glu Glu
 10 15 20 25

ttc atg gag cct ttg ggg ctg tcc caa aac ggc ttg gcg cgg gca ata 148
 Phe Met Glu Pro Leu Gly Leu Ser Gln Asn Gly Leu Ala Arg Ala Ile
 30 35 40

gga gtg cca cca cgc agg att aat gag atc gtg cac ggc aaa cgc gca 196
 Gly Val Pro Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys Arg Ala
 45 50 55

atc acg gca gac act gcg ctg cgt tta gct gct tat tta ggt ccc gat 244
 Ile Thr Ala Asp Thr Ala Leu Arg Leu Ala Ala Tyr Leu Gly Pro Asp
 60 65 70

cca cag ttt tgg ctc aac ttg cag acc cac tac gac ctg tcg gtg acg 292
 Pro Gln Phe Trp Leu Asn Leu Gln Thr His Tyr Asp Leu Ser Val Thr
 75 80 85

tat tta gat gcg cgc aca ctg ttg gaa gcg atc aag cct tat gat cgt 340
 Tyr Leu Asp Ala Arg Thr Leu Leu Glu Ala Ile Lys Pro Tyr Asp Arg
 90 95 100 105

cag caa aat gtg gct cgg acc ctg aat ccg ctt cag gag agc tcg cag 388
 Gln Gln Asn Val Ala Arg Thr Leu Asn Pro Leu Gln Glu Ser Ser Gln
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411

<210> 412

<211> 121

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

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 20 25 30

Ser Gln Asn Gly Leu Ala Arg Ala Ile Gly Val Pro Pro Arg Arg Ile
 35 40 45

Asn Glu Ile Val His Gly Lys Arg Ala Ile Thr Ala Asp Thr Ala Leu
 50 55 60

Arg Leu Ala Ala Tyr Leu Gly Pro Asp Pro Gln Phe Trp Leu Asn Leu
 65 70 75 80

Gln Thr His Tyr Asp Leu Ser Val Thr Tyr Leu Asp Ala Arg Thr Leu
 85 90 95

Leu Glu Ala Ile Lys Pro Tyr Asp Arg Gln Gln Asn Val Ala Arg Thr
 100 105 110

Leu Asn Pro Leu Gln Glu Ser Ser Gln
 115 120

<210> 413

<211> 381

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(358)

<223> RXA01149

<400> 413

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 Val Val Ala Pro Gln
 1 5

tcc cgg aaa ccg cag cac cct ggt gag att ttg agt gaa cgt ttc ctc 163
 Ser Arg Lys Pro Gln His Pro Gly Glu Ile Leu Ser Glu Arg Phe Leu
 10 15 20

gaa ccc cga gga atc agc cac tac gat ctc gcc aaa acc ctc cac atc 211
 Glu Pro Arg Gly Ile Ser His Tyr Asp Leu Ala Lys Thr Leu His Ile
 25 30 35

acc gaa gca acc atc gcc aat ttc gtt gaa ggt cgc acc gac ctc acc 259
 Thr Glu Ala Thr Ile Ala Asn Phe Val Glu Gly Arg Thr Asp Leu Thr
 40 45 50

atc gga ctt gca gta cgc ctc tcc cgc tca ttc gat ttg agc aca cag 307
 Ile Gly Leu Ala Val Arg Leu Ser Arg Ser Phe Asp Leu Ser Thr Gln
 55 60 65

gaa tgg atc gca ctg cag cgc acc ttt gat cag gct cat cgt cga tct 355
 Glu Trp Ile Ala Leu Gln Arg Thr Phe Asp Gln Ala His Arg Arg Ser
 70 75 80 85

gct taaaagtttt tagcttcac gaa 381
 Ala

<210> 414
 <211> 86
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 414
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Ser Glu Arg Phe Leu Glu Pro Arg Gly Ile Ser His Tyr Asp Leu Ala
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Lys Thr Leu His Ile Thr Glu Ala Thr Ile Ala Asn Phe Val Glu Gly
 35 40 45

Arg Thr Asp Leu Thr Ile Gly Leu Ala Val Arg Leu Ser Arg Ser Phe
 50 55 60

Asp Leu Ser Thr Gln Glu Trp Ile Ala Leu Gln Arg Thr Phe Asp Gln
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Ala His Arg Arg Ser Ala
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<210> 415
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 <223> RXA01305

<400> 415
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 Met Arg Pro Ser Ser
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cgg cca ctt ggc ctc gtc cta tgc acc gca ctg gca tca acg atc atc 163
 Arg Pro Leu Gly Leu Val Leu Cys Thr Ala Leu Ala Ser Thr Ile Ile

10										15					20					
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Thr Val Pro Ala Ala Ser Ala Gln Glu Pro Ala Leu Leu Asp Ala Ser																				
25 30 35																				
gcc atc gcc cca cat acc gcc agc tac ggc tac tac gtt gat gca tgg	259																			
Ala Ile Ala Pro His Thr Ala Ser Tyr Gly Tyr Tyr Val Asp Ala Trp																				
40 45 50																				
gac acc aac gtt tcc act gat ctg aat cca tca agt aat gca gct gtt	307																			
Asp Thr Asn Val Ser Thr Asp Leu Asn Pro Ser Ser Asn Ala Ala Val																				
55 60 65																				
ggc gta ctg gag gaa atg ctt gag ctg tgg acc cca ggc gaa gaa tgg	355																			
Gly Val Leu Glu Glu Met Leu Glu Leu Trp Thr Pro Gly Glu Glu Trp																				
70 75 80 85																				
aac acc ggc gtc aag gtt gac ccc acc gtg ctg gat tcc aac atc gca	403																			
Asn Thr Gly Val Lys Val Asp Pro Thr Val Leu Asp Ser Asn Ile Ala																				
90 95 100																				
cag tct gtg gca atc tcc cag cag gcg acc gat gct cag caa gaa cgt	451																			
Gln Ser Val Ala Ile Ser Gln Gln Ala Thr Asp Ala Gln Gln Glu Arg																				
105 110 115																				
gct tgg gtt att gat cgc cgc aac cag aac tac acc gca acc gac ggt	499																			
Ala Trp Val Ile Asp Arg Arg Asn Gln Asn Tyr Thr Ala Thr Asp Gly																				
120 125 130																				
ctt ggc gca tac gca gat agt tac cgc gag acc gca cag gtg ggc acc	547																			
Leu Gly Ala Tyr Ala Asp Ser Tyr Arg Glu Thr Ala Gln Val Gly Thr																				
135 140 145																				
acc atc cct gac gtt gtt cca gct gat gcc acc acc gtg aag tac aac	595																			
Thr Ile Pro Asp Val Val Pro Ala Asp Ala Thr Thr Val Lys Tyr Asn																				
150 155 160 165																				
gat ggc ggc aat gtg aat ggc aat tgg gca gag acc ggt gga gaa ctc	643																			
Asp Gly Gly Asn Val Asn Gly Asn Trp Ala Glu Thr Gly Gly Glu Leu																				
170 175 180																				
gga tcc act gtt gat cta att gaa gct atc cgt cag cat gcc gca acc	691																			
Gly Ser Thr Val Asp Leu Ile Glu Ala Ile Arg Gln His Ala Ala Thr																				
185 190 195																				
agc aac aat gcc aag gcg tac tac caa tac cca cgc ccc tac cgc tgg	739																			
Ser Asn Asn Ala Lys Ala Tyr Tyr Gln Tyr Pro Arg Pro Tyr Arg Trp																				
200 205 210																				
act gaa tcc atc gaa cca gaa gcc tgg ggc gag ggc gtt gac atg cca	787																			
Thr Glu Ser Ile Glu Pro Glu Ala Trp Gly Glu Gly Val Asp Met Pro																				
215 220 225																				
gag tat gca aac cca ctg cgc aag gat gaa tcc gaa gct gcc agc gat	835																			
Glu Tyr Ala Asn Pro Leu Arg Lys Asp Glu Ser Glu Ala Ala Ser Asp																				
230 235 240 245																				
ggc ggt ttc cct tcc gga cac acc tcc gca ggc ggc atg gca acc aac	883																			
Gly Gly Phe Pro Ser Gly His Thr Ser Ala Gly Gly Met Ala Thr Asn																				
250 255 260																				

ggc ctg gct tac gct ttc cca cag caa tac gat aaa ctg ctc atg act	931
Gly Leu Ala Tyr Ala Phe Pro Gln Gln Tyr Asp Lys Leu Leu Met Thr	
265 270 275	
gca gcg gaa atc ggc gaa agc cgc atc cag ctg ggc atg cac tct ccg	979
Ala Ala Glu Ile Gly Glu Ser Arg Ile Gln Leu Gly Met His Ser Pro	
280 285 290	
ctt gat gtt att ggc ggc cgt gtt cta tcc acc gcg att act gca ggt	1027
Leu Asp Val Ile Gly Gly Arg Val Leu Ser Thr Ala Ile Thr Ala Gly	
295 300 305	
gca ctt aat gat ccg aat ctc gac tcg gtg aag gct gaa gcc ttc gat	1075
Ala Leu Asn Asp Pro Asn Leu Asp Ser Val Lys Ala Glu Ala Phe Asp	
310 315 320 325	
gat gct cag gca tgg atc agt aac cag agc gac atc acc acc aac act	1123
Asp Ala Gln Ala Trp Ile Ser Asn Gln Ser Asp Ile Thr Thr Asn Thr	
330 335 340	
cgc gat ttt gat gag caa ctc gcc gag tac acc aac ttc ctc acc ttc	1171
Arg Asp Phe Asp Glu Gln Leu Ala Glu Tyr Thr Asn Phe Leu Thr Phe	
345 350 355	
ggc ttc gag cag tcc ggc gac acc acc caa gac atg cgc gtg cca aag	1219
Gly Phe Glu Gln Ser Gly Asp Thr Thr Gln Asp Met Arg Val Pro Lys	
360 365 370	
gga gct gag gct ctg ctg gaa acc cgc ctt ccg tac ctt gat gac gaa	1267
Gly Ala Glu Ala Leu Leu Glu Thr Arg Leu Pro Tyr Leu Asp Asp Glu	
375 380 385	
cag cgc cgt tgg gtt cta cat tcc act ggc ctc gag tcc ggt ttc cca	1315
Gln Arg Arg Trp Val Leu His Ser Thr Gly Leu Glu Ser Gly Phe Pro	
390 395 400 405	
gta ctt gat gat gcc gaa ggt tgg ggc cgt ctc aac ctc tac gct gcc	1363
Val Leu Asp Asp Ala Glu Gly Trp Gly Arg Leu Asn Leu Tyr Ala Ala	
410 415 420	
cag gct ggc tac agt gca ttc gat acc aac gtt gac gtc acc atg aat	1411
Gln Ala Gly Tyr Ser Ala Phe Asp Thr Asn Val Asp Val Thr Met Asn	
425 430 435	
gcc atc gac ggt ggc tac aac gcc aaa gac aac tgg caa aac gac atc	1459
Ala Ile Asp Gly Gly Tyr Asn Ala Lys Asp Asn Trp Gln Asn Asp Ile	
440 445 450	
gag ggc gca gga tcc ctg acc aag aac ggt tcc ggt gaa ctc acc ctg	1507
Glu Gly Ala Gly Ser Leu Thr Lys Asn Gly Ser Gly Glu Leu Thr Leu	
455 460 465	
tca ggt gac aac tcc tac acc ggt gga acc acc atc acc gcg ggc acc	1555
Ser Gly Asp Asn Ser Tyr Thr Gly Gly Thr Thr Ile Thr Ala Gly Thr	
470 475 480 485	
ttg gtt gct gca act gag tca gct ctg gga gca ggc gat ctc acc atc	1603
Leu Val Ala Ala Thr Glu Ser Ala Leu Gly Ala Gly Asp Leu Thr Ile	
490 495 500	

aac gat ggt gca acc ttg aag atc acc cag cct gtc acc gtg gat gga. 1651
 Asn Asp Gly Ala Thr Leu Lys Ile Thr Gln Pro Val Thr Val Asp Gly
 505 510 515

acc gca aac ctg gga gga act ctg cac gtt gcc ctt cct gtt ggc acc 1699
 Thr Ala Asn Leu Gly Gly Thr Leu His Val Ala Leu Pro Val Gly Thr
 520 525 530

aac cac gtc acc gtg atc gat gct gca tca att tcc ggt gaa ttt gat 1747
 Asn His Val Thr Val Ile Asp Ala Ala Ser Ile Ser Gly Glu Phe Asp
 535 540 545

gag gtt att gtt gat ggc gca gtt gac gct cag gtg agc tac gac aac 1795
 Glu Val Ile Val Asp Gly Ala Val Asp Ala Gln Val Ser Tyr Asp Asn
 550 555 560 565

ggc tct gtc gtg att act aca ggc gca cct tct gat gac gta aag gaa 1843
 Gly Ser Val Val Ile Thr Thr Gly Ala Pro Ser Asp Asp Val Lys Glu
 570 575 580

act ggc tct tct gct ggc gga att ctt gcc atc gtg gca gcc ctg ggt 1891
 Thr Gly Ser Ser Ala Gly Gly Ile Leu Ala Ile Val Ala Ala Leu Gly
 585 590 595

ggc att gca gca ctg atc ttc ggt gca ttc acc cag ttt ggt ttc cca 1939
 Gly Ile Ala Ala Leu Ile Phe Gly Ala Phe Thr Gln Phe Gly Phe Pro
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 Pro Ala Ile Lys Glu Met Phe Asp Leu
 615 620

ggc 1989

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 <213> Corynebacterium glutamicum

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Leu Leu Asp Ala Ser Ala Ile Ala Pro His Thr Ala Ser Tyr Gly Tyr
 35 40 45

Tyr Val Asp Ala Trp Asp Thr Asn Val Ser Thr Asp Leu Asn Pro Ser
 50 55 60

Ser Asn Ala Ala Val Gly Val Leu Glu Glu Met Leu Glu Leu Trp Thr
 65 70 75 80

Pro Gly Glu Glu Trp Asn Thr Gly Val Lys Val Asp Pro Thr Val Leu
 85 90 95

Asp Ser Asn Ile Ala Gln Ser Val Ala Ile Ser Gln Gln Ala Thr Asp
 100 105 110

Ala Gln Gln Glu Arg Ala Trp Val Ile Asp Arg Arg Asn Gln Asn Tyr
115 120 125

Thr Ala Thr Asp Gly Leu Gly Ala Tyr Ala Asp Ser Tyr Arg Glu Thr
130 135 140

Ala Gln Val Gly Thr Thr Ile Pro Asp Val Val Pro Ala Asp Ala Thr
145 150 155 160

Thr Val Lys Tyr Asn Asp Gly Gly Asn Val Asn Gly Asn Trp Ala Glu
165 170 175

Thr Gly Gly Glu Leu Gly Ser Thr Val Asp Leu Ile Glu Ala Ile Arg
180 185 190

Gln His Ala Ala Thr Ser Asn Asn Ala Lys Ala Tyr Tyr Gln Tyr Pro
195 200 205

Arg Pro Tyr Arg Trp Thr Glu Ser Ile Glu Pro Glu Ala Trp Gly Glu
210 215 220

Gly Val Asp Met Pro Glu Tyr Ala Asn Pro Leu Arg Lys Asp Glu Ser
225 230 235 240

Glu Ala Ala Ser Asp Gly Gly Phe Pro Ser Gly His Thr Ser Ala Gly
245 250 255

Gly Met Ala Thr Asn Gly Leu Ala Tyr Ala Phe Pro Gln Gln Tyr Asp
260 265 270

Lys Leu Leu Met Thr Ala Ala Glu Ile Gly Glu Ser Arg Ile Gln Leu
275 280 285

Gly Met His Ser Pro Leu Asp Val Ile Gly Gly Arg Val Leu Ser Thr
290 295 300

Ala Ile Thr Ala Gly Ala Leu Asn Asp Pro Asn Leu Asp Ser Val Lys
305 310 315 320

Ala Glu Ala Phe Asp Asp Ala Gln Ala Trp Ile Ser Asn Gln Ser Asp
325 330 335

Ile Thr Thr Asn Thr Arg Asp Phe Asp Glu Gln Leu Ala Glu Tyr Thr
340 345 350

Asn Phe Leu Thr Phe Gly Phe Glu Gln Ser Gly Asp Thr Thr Gln Asp
355 360 365

Met Arg Val Pro Lys Gly Ala Glu Ala Leu Leu Glu Thr Arg Leu Pro
370 375 380

Tyr Leu Asp Asp Glu Gln Arg Arg Trp Val Leu His Ser Thr Gly Leu
385 390 395 400

Glu Ser Gly Phe Pro Val Leu Asp Asp Ala Glu Gly Trp Gly Arg Leu
405 410 415

Asn Leu Tyr Ala Ala Gln Ala Gly Tyr Ser Ala Phe Asp Thr Asn Val
420 425 430

Asp Val Thr Met Asn Ala Ile Asp Gly Gly Tyr Asn Ala Lys Asp Asn
 435 440 445
 Trp Gln Asn Asp Ile Glu Gly Ala Gly Ser Leu Thr Lys Asn Gly Ser
 450 455 460
 Gly Glu Leu Thr Leu Ser Gly Asp Asn Ser Tyr Thr Gly Gly Thr Thr
 465 470 475 480
 Ile Thr Ala Gly Thr Leu Val Ala Ala Thr Glu Ser Ala Leu Gly Ala
 485 490 495
 Gly Asp Leu Thr Ile Asn Asp Gly Ala Thr Leu Lys Ile Thr Gln Pro
 500 505 510
 Val Thr Val Asp Gly Thr Ala Asn Leu Gly Gly Thr Leu His Val Ala
 515 520 525
 Leu Pro Val Gly Thr Asn His Val Thr Val Ile Asp Ala Ala Ser Ile
 530 535 540
 Ser Gly Glu Phe Asp Glu Val Ile Val Asp Gly Ala Val Asp Ala Gln
 545 550 555 560
 Val Ser Tyr Asp Asn Gly Ser Val Val Ile Thr Thr Gly Ala Pro Ser
 565 570 575
 Asp Asp Val Lys Glu Thr Gly Ser Ser Ala Gly Gly Ile Leu Ala Ile
 580 585 590
 Val Ala Ala Leu Gly Gly Ile Ala Ala Leu Ile Phe Gly Ala Phe Thr
 595 600 605
 Gln Phe Gly Phe Pro Pro Ala Ile Lys Glu Met Phe Asp Leu
 610 615 620

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 <211> 420
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(397)
 <223> RXA01453

<400> 417
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 Met Ala Gln Lys Leu
 1 5
 tac ccg ccg att cac cct ggt gag att ctc atg gag gac ttc atc aag 163
 Tyr Pro Pro Ile His Pro Gly Glu Ile Leu Met Glu Asp Phe Ile Lys
 10 15 20
 ggc ttc ggc ctc aca cag aac aag gtc gcc gta tcg atc ggg gtg cct 211
 Gly Phe Gly Leu Thr Gln Asn Lys Val Ala Val Ser Ile Gly Val Pro
 25 30 35

ccg cga cgc atc aac gag atc gtg cac ggc aag cga tcc atc acg gcc 259
Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys Arg Ser Ile Thr Ala
40 45 50

gat acg gct ctg cgt ctc ggg cgg tac ttc ggt atc gac ccg cag ttc 307
Asp Thr Ala Leu Arg Leu Gly Arg Tyr Phe Gly Ile Asp Pro Gln Phe
55 60 65

tgg ctg agc ctt cag act cag tac gag ttg gag ctc gat cgc gac gcc 355
Trp Leu Ser Leu Gln Thr Gln Tyr Glu Leu Glu Leu Asp Arg Asp Ala
70 75 80 85

ggt gca gcg act tac gca cag atc acg ccg ctg aag gtc gcg 397
Gly Ala Ala Thr Tyr Ala Gln Ile Thr Pro Leu Lys Val Ala
90 95

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<400> 418
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Ser Ile Gly Val Pro Pro Arg Arg Ile Asn Glu Ile Val His Gly Lys
35 40 45

Arg Ser Ile Thr Ala Asp Thr Ala Leu Arg Leu Gly Arg Tyr Phe Gly
50 55 60

Ile Asp Pro Gln Phe Trp Leu Ser Leu Gln Thr Gln Tyr Glu Leu Glu
65 70 75 80

Leu Asp Arg Asp Ala Gly Ala Ala Thr Tyr Ala Gln Ile Thr Pro Leu
85 90 95

Lys Val Ala

<210> 419
<211> 945
<212> DNA
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<220>
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acggccgacc actcatcgtg cccacagaca ggagaaactc	atg aaa gaa acc gac	115
	Met Lys Glu Thr Asp	
	1 5	
aac cta ctg cgc gaa aac tcc cac gac cgc gac atc tct gaa atc gtc	163	
Asn Leu Leu Arg Glu Asn Ser His Asp Arg Asp Ile Ser Glu Ile Val		
10 15 20		
gcc acc atc act gcc ctt gac cac cca tca ccc tca ctt ctg cga ttc	211	
Ala Thr Ile Thr Ala Leu Asp His Pro Ser Pro Ser Leu Leu Arg Phe		
25 30 35		
aca gct ttt gtt cca gga tca gca aac aac cca gtg tgg gca gaa gcc	259	
Thr Ala Phe Val Pro Gly Ser Ala Asn Asn Pro Val Trp Ala Glu Ala		
40 45 50		
aac gtg gca atc agg ctt tac ctc agc gaa gaa ttc gac gac gcc acc	307	
Asn Val Ala Ile Arg Leu Tyr Leu Ser Glu Glu Phe Asp Asp Ala Thr		
55 60 65		
cgc gtc tac acc gtc cga tcc ttt gat gcc gca act gaa agc atc gtg	355	
Arg Val Tyr Thr Val Arg Ser Phe Asp Ala Ala Thr Glu Ser Ile Val		
70 75 80 85		
gtg gat gtg gtt caa cac cac cac gaa agc ccc atg atg cgc tgg tca	403	
Val Asp Val Val Gln His His His Glu Ser Pro Met Met Arg Trp Ser		
90 95 100		
gac acc gta aaa atc aac gac acc ctc gtg ctc acc gga ccc cgc cca	451	
Asp Thr Val Lys Ile Asn Asp Thr Leu Val Leu Thr Gly Pro Arg Pro		
105 110 115		
cac ttt gtc atc ccc gaa ggc gaa caa gca gca ctc ttc ctt gat gac	499	
His Phe Val Ile Pro Glu Gly Glu Gln Ala Ala Leu Phe Leu Asp Asp		
120 125 130		
acc gcc atc ccc gct ctc gcc gct att ttg gat caa tgg cca aca gat	547	
Thr Ala Ile Pro Ala Leu Ala Ala Ile Leu Asp Gln Trp Pro Thr Asp		
135 140 145		
ctt cgt ggc aaa gga tgg gtt gtc act gac gat ccc gca gcc ttc gat	595	
Leu Arg Gly Lys Gly Trp Val Val Thr Asp Asp Pro Ala Ala Phe Asp		
150 155 160 165		
gaa cta ccc agc atc gac gga ctg gaa ctg aac ctg ctc gcg ccg gga	643	
Glu Leu Pro Ser Ile Asp Gly Leu Glu Leu Asn Leu Leu Ala Pro Gly		
170 175 180		
tca gat cca act gtt cag cca ctt gcc caa cag gca tat gac ctg gaa	691	
Ser Asp Pro Thr Val Gln Pro Leu Ala Gln Gln Ala Tyr Asp Leu Glu		
185 190 195		
aac cca gaa act tac gtg gtg tgg gca gcc ggc gag cga gat gaa ata	739	
Asn Pro Glu Thr Tyr Val Val Trp Ala Ala Gly Glu Arg Asp Glu Ile		
200 205 210		
aaa tcc atc cgc agg cac ttc cgc aag cag gtg gga ttg gaa aaa gat	787	
Lys Ser Ile Arg Arg His Phe Arg Lys Gln Val Gly Leu Glu Lys Asp		
215 220 225		
gca gtg gcc gtg ttt ggg tac tgg aaa tac aac acc acc aac act cag	835	

Ala Val Ala Val Phe Gly Tyr Trp Lys Tyr Asn Thr Thr Asn Thr Gln
 230 235 240 245

atc gat gca gtc cgc aaa gaa aac tac atg aag atg ctc tct gaa ggg 883
 Ile Asp Ala Val Arg Lys Glu Asn Tyr Met Lys Met Leu Ser Glu Gly
 250 255 260

cta cag ctg gaa aac ttc gac gac ctc tca ttg gag att taaggggtcg 932
 Leu Gln Leu Glu Asn Phe Asp Asp Leu Ser Leu Glu Ile
 265 270

agtttttaga atg 945

<210> 420

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

Met Lys Glu Thr Asp Asn Leu Leu Arg Glu Asn Ser His Asp Arg Asp
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Ile Ser Glu Ile Val Ala Thr Ile Thr Ala Leu Asp His Pro Ser Pro
 20 25 30

Ser Leu Leu Arg Phe Thr Ala Phe Val Pro Gly Ser Ala Asn Asn Pro
 35 40 45

Val Trp Ala Glu Ala Asn Val Ala Ile Arg Leu Tyr Leu Ser Glu Glu
 50 55 60

Phe Asp Asp Ala Thr Arg Val Tyr Thr Val Arg Ser Phe Asp Ala Ala
 65 70 75 80

Thr Glu Ser Ile Val Val Asp Val Val Gln His His His Glu Ser Pro
 85 90 95

Met Met Arg Trp Ser Asp Thr Val Lys Ile Asn Asp Thr Leu Val Leu
 100 105 110

Thr Gly Pro Arg Pro His Phe Val Ile Pro Glu Gly Glu Gln Ala Ala
 115 120 125

Leu Phe Leu Asp Asp Thr Ala Ile Pro Ala Leu Ala Ala Ile Leu Asp
 130 135 140

Gln Trp Pro Thr Asp Leu Arg Gly Lys Gly Trp Val Val Thr Asp Asp
 145 150 155 160

Pro Ala Ala Phe Asp Glu Leu Pro Ser Ile Asp Gly Leu Glu Leu Asn
 165 170 175

Leu Leu Ala Pro Gly Ser Asp Pro Thr Val Gln Pro Leu Ala Gln Gln
 180 185 190

Ala Tyr Asp Leu Glu Asn Pro Glu Thr Tyr Val Val Trp Ala Ala Gly
 195 200 205

Glu Arg Asp Glu Ile Lys Ser Ile Arg Arg His Phe Arg Lys Gln Val
 210 215 220

Gly Leu Glu Lys Asp Ala Val Ala Val Phe Gly Tyr Trp Lys Tyr Asn
225 230 235 240

Thr Thr Asn Thr Gln Ile Asp Ala Val Arg Lys Glu Asn Tyr Met Lys
245 250 255

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Glu Ile

<210> 421

<211> 1017

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(994)

<223> RXA01832

<400> 421

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Met Ala Thr Ser Asn
1 5

cgg ata gct aat gct atg aac agt ttg gcc aag ctg gac agt tct atg 163
Arg Ile Ala Asn Ala Met Asn Ser Leu Ala Lys Leu Asp Ser Ser Met
10 15 20

caa cgc ggc ctt gat aat gcg ttg gcg ttt gtt ttc cgt ggt cgc gtt 211
Gln Arg Gly Leu Asp Asn Ala Leu Ala Phe Val Phe Arg Gly Arg Val
25 30 35

gtt ccg gct gag ctt gag gag ctt ttg aag caa gag gct gag gac aat 259
Val Pro Ala Glu Leu Glu Glu Leu Lys Gln Glu Ala Glu Asp Asn
40 45 50

gtg gtt cat act gag ttt ggc tat gtt gag gcg ccg aat gtt ttt aag 307
Val Val His Thr Glu Phe Gly Tyr Val Glu Ala Pro Asn Val Phe Lys
55 60 65

gtt tcg gtg agc ccg aac gat ttt agt aat ctt gtc gat cgt ttt cct 355
Val Ser Val Ser Pro Asn Asp Phe Ser Asn Leu Val Asp Arg Phe Pro
70 75 80 85

gat cag ccg gct cgt ttt ggt gat cag atg atg agg ttc tgc agg aac 403
Asp Gln Pro Ala Arg Phe Gly Asp Gln Met Met Arg Phe Cys Arg Asn
90 95 100

agt ggc tgg acg ttg gtt ggg ccg gtg att gtg ttg att gaa gag gat 451
Ser Gly Trp Thr Leu Val Gly Pro Val Ile Val Leu Ile Glu Glu Asp
105 110 115

tct tcg ttg cac acg ggc cag ttg aag tcg gtt tcg gag aag gat ccg 499
Ser Ser Leu His Thr Gly Gln Leu Lys Ser Val Ser Glu Lys Asp Pro

120	125	130	
gat ccg gag tta agt agc ggt tat ctg cct ttg gaa ggc gac ggc atc			547
Asp Pro Glu Leu Ser Ser Gly Tyr Leu Pro Leu Glu Gly Asp Gly Ile			
135	140	145	
ctg cct gtc gca gaa agt gag tct aag aac gtg tct gac agt tcc cct			595
Leu Pro Val Ala Glu Ser Glu Ser Lys Asn Val Ser Asp Ser Ser Pro			
150	155	160	165
tac act ggt acg gag ttt ttg ccg gcg caa tca gcg gat cgc cct ttg			643
Tyr Thr Gly Thr Glu Phe Leu Pro Ala Gln Ser Ala Asp Arg Pro Leu			
170	175		180
gtt cag ggt gtg ccg cag tct cag gtt gat gcg aat cgc cag gct gcg			691
Val Gln Gly Val Pro Gln Ser Gln Val Asp Ala Asn Arg Gln Ala Ala			
185	190		195
atg aag ccc gcg ggc cct acg gtg act ttg ctg ctg cag gat ggt tcg			739
Met Lys Pro Ala Gly Pro Thr Val Thr Leu Leu Leu Gln Asp Gly Ser			
200	205		210
agc cgg act tat ttg gtt ccg gag ggt tcg aac atc att ggt cgt agt			787
Ser Arg Thr Tyr Leu Val Arg Glu Gly Ser Asn Ile Ile Gly Arg Ser			
215	220		225
aat gat gcg gat ctt cgt ttg ccg gat act ggt gtg tct cgt cag cat			835
Asn Asp Ala Asp Leu Arg Leu Pro Asp Thr Gly Val Ser Arg Gln His			
230	235	240	245
gtg gag atc acg tgg gat ggc ccg gat gcc att ttg gtt gat ttg aag			883
Val Glu Ile Thr Trp Asp Gly Arg Asp Ala Ile Leu Val Asp Leu Lys			
250	255		260
tcg act aat ggc acc acg gtg aat gac act cct gtg gat aat tgg ttg			931
Ser Thr Asn Gly Thr Thr Val Asn Asp Thr Pro Val Asp Asn Trp Leu			
265	270		275
ttg gct gat ggt gat gtc att acg gtg ggt cat tcc aat atc gaa gtt			979
Leu Ala Asp Gly Asp Val Ile Thr Val Gly His Ser Asn Ile Glu Val			
280	285		290
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Arg Ile Val Ser Pro			
295			

<210> 422

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

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	20						25					30			

Phe	Arg	Gly	Arg	Val	Val	Pro	Ala	Glu	Leu	Glu	Glu	Leu	Leu	Lys	Gln
	35						40					45			

Glu Ala Glu Asp Asn Val Val His Thr Glu Phe Gly Tyr Val Glu Ala
50 55 60

Pro Asn Val Phe Lys Val Ser Val Ser Pro Asn Asp Phe Ser Asn Leu
65 70 75 80

Val Asp Arg Phe Pro Asp Gln Pro Ala Arg Phe Gly Asp Gln Met Met
85 90 95

Arg Phe Cys Arg Asn Ser Gly Trp Thr Leu Val Gly Pro Val Ile Val
100 105 110

Leu Ile Glu Glu Asp Ser Ser Leu His Thr Gly Gln Leu Lys Ser Val
115 120 125

Ser Glu Lys Asp Pro Asp Pro Glu Leu Ser Ser Gly Tyr Leu Pro Leu
130 135 140

Glu Gly Asp Gly Ile Leu Pro Val Ala Glu Ser Glu Ser Lys Asn Val
145 150 155 160

Ser Asp Ser Ser Pro Tyr Thr Gly Thr Glu Phe Leu Pro Ala Gln Ser
165 170 175

Ala Asp Arg Pro Leu Val Gln Gly Val Pro Gln Ser Gln Val Asp Ala
180 185 190

Asn Arg Gln Ala Ala Met Lys Pro Ala Gly Pro Thr Val Thr Leu Leu
195 200 205

Leu Gln Asp Gly Ser Ser Arg Thr Tyr Leu Val Arg Glu Gly Ser Asn
210 215 220

Ile Ile Gly Arg Ser Asn Asp Ala Asp Leu Arg Leu Pro Asp Thr Gly
225 230 235 240

Val Ser Arg Gln His Val Glu Ile Thr Trp Asp Gly Arg Asp Ala Ile
245 250 255

Leu Val Asp Leu Lys Ser Thr Asn Gly Thr Thr Val Asn Asp Thr Pro
260 265 270

Val Asp Asn Trp Leu Leu Ala Asp Gly Asp Val Ile Thr Val Gly His
275 280 285

Ser Asn Ile Glu Val Arg Ile Val Ser Pro
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<211> 690

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(667)

<223> RXA02533

<400> 423

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<213> Corynebacterium glutamicum
<400> 424
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<400> 424

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 Val Ser Arg Ala Met Ile Ser Arg Val Glu Asn Ala Glu Ala Gln Pro
 35 40 45
 Ser Ala Ala Leu Leu Gly Arg Leu Ser Gly Ala Leu Gly Met Thr Leu
 50 55 60
 Ser Glu Leu Ile Ala Gln Ala Glu Gly Gly Tyr Asp Arg Gly Ala Arg
 65 70 75 80
 Arg Ser Lys Gln Ser Val Trp Thr Asp Pro Ala Thr Gly Tyr Thr Arg
 85 90 95
 Arg Ala Val Ser Gln Pro Ser Glu Ser Pro Leu Glu Leu Val Glu Val
 100 105 110
 Met Leu Pro Pro Gly Ala Glu Val Gly Tyr Pro Ala Asp Ala Tyr Arg
 115 120 125
 Phe Met Asp Gln Val Val Trp Val Leu Glu Gly Ala Val Arg Ile Thr
 130 135 140
 Glu Gly Glu Glu Val His Glu Leu Ser Thr Gly Asp Cys Leu Arg Phe
 145 150 155 160
 Gly Pro Pro Arg Asp Thr Asp Phe Ala Asn Pro Thr Thr Val Ala Thr
 165 170 175
 Arg Tyr Leu Val Ala Leu Asp Lys Arg Val Pro Arg Ala
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<210> 425

<211> 1035

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1012)

<223> RXN02727

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 Val Val Leu Leu Pro 5
 1

ctg cta gtt cct caa ctg cag gtg cag cca cag ttg cag ctt cca agt 163
 Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln Leu Gln Leu Pro Ser 20
 10 15

ctg ttg acg agg cag cgc tgc gca agg aaa tca aag aga agc tgc gct 211
 Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser Lys Arg Ser Cys Ala 35
 25 30

ccg aat acg gca tcc aag ctc gat gat gcc tcc aag gcc gct cag aag	259
Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser Lys Ala Ala Gln Lys	
40 45 50	
gct caa aac gat gcg aag tcc gct caa gat cag cta cag cgt gca caa	307
Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln Leu Gln Arg Ala Gln	
55 60 65	
gct gac gca aag gca gct cgc gac gaa gct gaa aag gcc aag gct gaa	355
Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu Lys Ala Lys Ala Glu	
70 75 80 85	
gct aag tca gca gca tcc tcc agc acc act aag gca gca gcg gtt ggc	403
Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys Ala Ala Ala Val Gly	
90 95 100	
gct gtc ggc gct ggc acc gga gca gca gtt gct aca ggt gct gca aat	451
Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala Thr Gly Ala Ala Asn	
105 110 115	
gtg gac acc cac atg cag gca gcg aag gtt ctg gga ctc gca cag gaa	499
Val Asp Thr His Met Gln Ala Ala Lys Val Leu Gly Leu Ala Gln Glu	
120 125 130	
atg gca gac cgc ctg acc tca gag gct cgc tcc gaa tcc aag tcc atg	547
Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser Glu Ser Lys Ser Met	
135 140 145	
ctg gac gag gct cgc gaa gca gca gag aag cag atc gag gaa gca aac	595
Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln Ile Glu Glu Ala Asn	
150 155 160 165	
agc acc tcc aac cgc act ctg gaa gat gct cgc gca aac gct gag aag	643
Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg Ala Asn Ala Glu Lys	
170 175 180	
cag atc gct gaa gcg cag aac cgc gct gac act ctg gtc aac gaa gct	691
Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr Leu Val Asn Glu Ala	
185 190 195	
gac gct aag gct aag aac ctg gtt tcc gaa gcc gag aag aag tcc gca	739
Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala Glu Lys Lys Ser Ala	
200 205 210	
gcc acc ctg gcc gca tcc acc tct cgt gca gaa gct cag atc cgt caa	787
Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu Ala Gln Ile Arg Gln	
215 220 225	
gcc gag gac aag gca aac gcc ctc cag gca gac gca gag cgc aag cac	835
Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp Ala Glu Arg Lys His	
230 235 240 245	
acc gaa acc atg gct gca gtc aag gaa cag cag aat gct ctg gag acc	883
Thr Glu Thr Met Ala Ala Val Lys Glu Gln Gln Asn Ala Leu Glu Thr	
250 255 260	
cgc atc gcg gaa ctg cag acc ttc gag cgt gag tac cgc acc cgt ctg	931
Arg Ile Ala Glu Leu Gln Thr Phe Glu Arg Glu Tyr Arg Thr Arg Leu	
265 270 275	

aag tcc ctc ctc gag ggc cag ctg gaa gaa ctc cac gca cgt ggc tcc 979
Lys Ser Leu Leu Glu Gly Gln Leu Glu Glu Leu His Ala Arg Gly Ser
280 285 290

tct gca cca acc aac aac aag cca tct ggt gag taaaaagaaa gattagttat 1032
Ser Ala Pro Thr Asn Asn Lys Pro Ser Gly Glu
295 300

ctt 1035

<210> 426
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 426
Val Val Leu Leu Pro Leu Leu Val Pro Gln Leu Gln Val Gln Pro Gln
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Leu Gln Leu Pro Ser Leu Leu Thr Arg Gln Arg Cys Ala Arg Lys Ser
20 25 30
Lys Arg Ser Cys Ala Pro Asn Thr Ala Ser Lys Leu Asp Asp Ala Ser
35 40 45
Lys Ala Ala Gln Lys Ala Gln Asn Asp Ala Lys Ser Ala Gln Asp Gln
50 55 60
Leu Gln Arg Ala Gln Ala Asp Ala Lys Ala Ala Arg Asp Glu Ala Glu
65 70 75 80
Lys Ala Lys Ala Glu Ala Lys Ser Ala Ala Ser Ser Ser Thr Thr Lys
85 90 95
Ala Ala Ala Val Gly Ala Val Gly Ala Gly Thr Gly Ala Ala Val Ala
100 105 110
Thr Gly Ala Ala Asn Val Asp Thr His Met Gln Ala Ala Lys Val Leu
115 120 125
Gly Leu Ala Gln Glu Met Ala Asp Arg Leu Thr Ser Glu Ala Arg Ser
130 135 140
Glu Ser Lys Ser Met Leu Asp Glu Ala Arg Glu Ala Ala Glu Lys Gln
145 150 155 160
Ile Glu Glu Ala Asn Ser Thr Ser Asn Arg Thr Leu Glu Asp Ala Arg
165 170 175
Ala Asn Ala Glu Lys Gln Ile Ala Glu Ala Gln Asn Arg Ala Asp Thr
180 185 190
Leu Val Asn Glu Ala Asp Ala Lys Ala Lys Asn Leu Val Ser Glu Ala
195 200 205
Glu Lys Lys Ser Ala Ala Thr Leu Ala Ala Ser Thr Ser Arg Ala Glu
210 215 220
Ala Gln Ile Arg Gln Ala Glu Asp Lys Ala Asn Ala Leu Gln Ala Asp
225 230 235 240

<400> 427																
gctgtttttt gatgcattcca tgataggaat agagcctagt gcatgatggc tgattttcct																60
gttaggtgcc accgacccca gtgatgataa cttgattgtc atg aaa tcc att gat																115
Met Lys Ser Ile Asp																5
1																
ctt gag cag ctg gcg ggc acg caa tcg cgc acg tat caa tcg cga aag																163
Leu Glu Gln Leu Ala Gly Thr Gln Ser Arg Thr Tyr Gln Ser Arg Lys																20
10 15																
atc acc gat gag atg gtc gcc cgg ccg gtg cat gtg gcg atc gcg ctg																211
Ile Thr Asp Glu Met Val Ala Arg Pro Val His Val Ala Ile Ala Leu																35
25 30																
tgg gaa gtg ccg tgg gag tcg gca aaa tcc ggc aag att gag ggt tgg																259
Trp Glu Val Pro Trp Glu Ser Ala Lys Ser Gly Lys Ile Glu Gly Trp																50
40 45																
gtc att gcc gtg gat tcg ccg cgt ggg ccg ttt gtg cgc agc ggg cag																307
Val Ile Ala Val Asp Ser Pro Arg Gly Arg Phe Val Arg Ser Gly Gln																65
55 60																
acc aaa aat ggc gac gcc gtc aac ccg act gtg tcg atg ctg aaa tca																355
Thr Lys Asn Gly Asp Ala Val Asn Arg Thr Val Ser Met Leu Lys Ser																85
70 75 80																
gcg ttg aaa ggg gtc cgc ggg aag gcg tgg att gta act ggg cgt cga																403
Ala Leu Lys Gly Val Arg Gly Lys Ala Trp Ile Val Thr Gly Arg Arg																100
90 95 100																
caa gca gct tta cgc gca gcc ctg gtg cgc gaa aac tac ctg gtc acc																451
Gln Ala Ala Leu Arg Ala Ala Leu Val Arg Glu Asn Tyr Leu Val Thr																115
105 110																

gga agc ttc gcc gag caa aat agg gcc ggc gtg aag gcg tcg gcg atc Gly Ser Phe Ala Glu Gln Asn Arg Ala Gly Val Lys Ala Ser Ala Ile 120 125 130	499
tcg cgc cgc gcc gaa caa tcc gcg ctg tac aag gcg aaa aaa atc ggc Ser Arg Arg Ala Glu Gln Ser Ala Leu Tyr Lys Ala Lys Lys Ile Gly 135 140 145	547
gaa ttc gcc gag cgc gcc cca cgc gtc aaa gag cgg caa gag gca cat Glu Phe Ala Glu Arg Ala Pro Arg Val Lys Glu Arg Gln Glu Ala His 150 155 160 165	595
tgg tgg cca cgg ttg tca cgc acg caa ggc acc gca ggc gtt tta cgc Trp Trp Pro Arg Leu Ser Arg Thr Gln Gly Thr Ala Gly Val Leu Arg 170 175 180	643
tta gcg acg gac gcc tct acc gat ggg gtc ttc cgc ggc gcc atg tgc Leu Ala Thr Asp Ala Ser Thr Asp Gly Val Phe Arg Gly Ala Met Cys 185 190 195	691
ttc gta gcc tca aac ggc gac tac ctg ctg gag acc caa gac acc acc Phe Val Ala Ser Asn Gly Asp Tyr Leu Leu Glu Thr Gln Asp Thr Thr 200 205 210	739
gca agc tcc gac gaa tta gaa ctg gaa agc atc acc cac gcc ctg atc Ala Ser Ser Asp Glu Leu Glu Leu Glu Ser Ile Thr His Ala Leu Ile 215 220 225	787
tac ctg aaa acc atc ggc gcg acc caa gcc atc atc gaa tcc gac agc Tyr Leu Lys Thr Ile Gly Ala Thr Gln Ala Ile Ile Glu Ser Asp Ser 230 235 240 245	835
aaa gcc gca ctt gaa gcc atc gac ttc atc ctg aac aac cga ccg cgc Lys Ala Ala Leu Glu Ala Ile Asp Phe Ile Leu Asn Asn Arg Pro Arg 250 255 260	883
cgg ggc agg tgg cgc ggc atc acc gca tgc gcc cgc aac cgg ttc cgg Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala Arg Asn Arg Phe Arg 265 270 275	931
gat gcc tgg gaa gcg ctt atc gac gac tgc gtt gtg gaa tta tcc cgc Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val Val Glu Leu Ser Arg 280 285 290	979
gta cta ggg cac gcc ggg gat cca ctg aac caa gca gcc gac caa atc Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln Ala Ala Asp Gln Ile 295 300 305	1027
gca tac atg ggc atg cgc gcc gta att ttt gaa caa aaa tcc gca cac Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu Gln Lys Ser Ala His 310 315 320 325	1075
ccc aca ttg ctg aaa gga att gac aag gcg ctt cgc aag gcc gag Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu Arg Lys Ala Glu 330 335 340	1120
taaggtgggc aacgagtcgg tga	1143

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 428

Met Lys Ser Ile Asp Leu Glu Gln Leu Ala Gly Thr Gln Ser Arg Thr
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Tyr Gln Ser Arg Lys Ile Thr Asp Glu Met Val Ala Arg Pro Val His
20 25 30
Val Ala Ile Ala Leu Trp Glu Val Pro Trp Glu Ser Ala Lys Ser Gly
35 40 45
Lys Ile Glu Gly Trp Val Ile Ala Val Asp Ser Pro Arg Gly Arg Phe
50 55 60
Val Arg Ser Gly Gln Thr Lys Asn Gly Asp Ala Val Asn Arg Thr Val
65 70 75 80
Ser Met Leu Lys Ser Ala Leu Lys Gly Val Arg Gly Lys Ala Trp Ile
85 90 95
Val Thr Gly Arg Arg Gln Ala Ala Leu Arg Ala Ala Leu Val Arg Glu
100 105 110
Asn Tyr Leu Val Thr Gly Ser Phe Ala Glu Gln Asn Arg Ala Gly Val
115 120 125
Lys Ala Ser Ala Ile Ser Arg Arg Ala Glu Gln Ser Ala Leu Tyr Lys
130 135 140
Ala Lys Lys Ile Gly Glu Phe Ala Glu Arg Ala Pro Arg Val Lys Glu
145 150 155 160
Arg Gln Glu Ala His Trp Trp Pro Arg Leu Ser Arg Thr Gln Gly Thr
165 170 175
Ala Gly Val Leu Arg Leu Ala Thr Asp Ala Ser Thr Asp Gly Val Phe
180 185 190
Arg Gly Ala Met Cys Phe Val Ala Ser Asn Gly Asp Tyr Leu Leu Glu
195 200 205
Thr Gln Asp Thr Thr Ala Ser Ser Asp Glu Leu Glu Leu Glu Ser Ile
210 215 220
Thr His Ala Leu Ile Tyr Leu Lys Thr Ile Gly Ala Thr Gln Ala Ile
225 230 235 240
Ile Glu Ser Asp Ser Lys Ala Ala Leu Glu Ala Ile Asp Phe Ile Leu
245 250 255
Asn Asn Arg Pro Arg Arg Gly Arg Trp Arg Gly Ile Thr Ala Cys Ala
260 265 270
Arg Asn Arg Phe Arg Asp Ala Trp Glu Ala Leu Ile Asp Asp Cys Val
275 280 285
Val Glu Leu Ser Arg Val Leu Gly His Ala Gly Asp Pro Leu Asn Gln
290 295 300

Ala Ala Asp Gln Ile Ala Tyr Met Gly Met Arg Ala Val Ile Phe Glu
305 310 315 320

Gln Lys Ser Ala His Pro Thr Leu Leu Lys Gly Ile Asp Lys Ala Leu
325 330 335

Arg Lys Ala Glu
340

<210> 429

<211> 780

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> RXN01966

<400> 429

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tatgggctgg gtttataaga agatgggtta gtttttaaaa gtg tct gaa tct gaa 115
Val Ser Glu Ser Glu
1 5
aac aac aca aca cca gca gtc gca gct cgc gat gac cgt ctg gtc tgg 163
Asn Asn Thr Thr Pro Ala Val Ala Ala Arg Asp Asp Arg Leu Val Trp
10 15 20
gtc gat ctg gaa atg act ggt cta gat ttg aag cgc cac gtg atc gtg 211
Val Asp Leu Glu Met Thr Gly Leu Asp Leu Lys Arg His Val Ile Val
25 30 35
gag gtt gcg gcg ttg gtc act gac gct aac ctc aac gtt ttg ggc gag 259
Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu Asn Val Leu Gly Glu
40 45 50
ggc gtg gac ttg gtt gtt cac gca act gaa gaa gag ctc gcg cag atg 307
Gly Val Asp Leu Val Val His Ala Thr Glu Glu Glu Leu Ala Gln Met
55 60 65
gat gat ttt gtc acc aac atg cac gaa tcc tct ggg ctg act gag cag 355
Asp Asp Phe Val Thr Asn Met His Glu Ser Ser Gly Leu Thr Glu Gln
70 75 80 85
atc cgg gaa tcc gcg gtc acg ttg aag gaa gcc gaa gat gct gtg ctc 403
Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala Glu Asp Ala Val Leu
90 95 100
gca ttg att gaa aag cac tgc gat cca gcc cat cct gca ccg cta gct 451
Ala Leu Ile Glu Lys His Cys Asp Pro Ala His Pro Ala Pro Leu Ala
105 110 115
ggg aac tcc att gcc act gac cgc gcg ttt atc cgc gaa cat atg cca 499
Gly Asn Ser Ile Ala Thr Asp Arg Ala Phe Ile Arg Glu His Met Pro
120 125 130
cgt ctt gat gag gcc ctg cat tac cgc atg gtg gat gtg tcc tcg gtg 547

Arg Leu Asp Glu Ala Leu His Tyr Arg Met Val Asp Val Ser Ser Val
 135 140 145
 aag gaa ttg gcg cgt cgc tgg tac cca cgc gtg tac tac aag cag ccg 595
 Lys Glu Leu Ala Arg Arg Trp Tyr Pro Arg Val Tyr Tyr Lys Gln Pro
 150 155 160 165
 gag aag ggt ttg gcg cac cgc gcg ttg gcg gac att gtg gag tcg att 643
 Glu Lys Gly Leu Ala His Arg Ala Leu Ala Asp Ile Val Glu Ser Ile
 170 175 180
 cgg gag ttg gat tac tac cgt cgc tca ttt ttt gtt gca gag cct ggt 691
 Arg Glu Leu Asp Tyr Tyr Arg Arg Ser Phe Phe Val Ala Glu Pro Gly
 185 190 195
 cct acc tct gag cag tgc gca gat gat gcg cag gca gcg gtg gac cgt 739
 Pro Thr Ser Glu Gln Cys Ala Asp Ala Gln Ala Val Asp Arg
 200 205 210
 ttt gca ccc tac ttt gat tagagggttt taagcagcct ggt 780
 Phe Ala Pro Tyr Phe Asp
 215

<210> 430

<211> 219

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 430

Val Ser Glu Ser Glu Asn Asn Thr Thr Pro Ala Val Ala Ala Arg Asp
 1 5 10 15
 Asp Arg Leu Val Trp Val Asp Leu Glu Met Thr Gly Leu Asp Leu Lys
 20 25 30
 Arg His Val Ile Val Glu Val Ala Ala Leu Val Thr Asp Ala Asn Leu
 35 40 45
 Asn Val Leu Gly Glu Gly Val Asp Leu Val Val His Ala Thr Glu Glu
 50 55 60
 Glu Leu Ala Gln Met Asp Asp Phe Val Thr Asn Met His Glu Ser Ser
 65 70 75 80
 Gly Leu Thr Glu Gln Ile Arg Glu Ser Ala Val Thr Leu Lys Glu Ala
 85 90 95
 Glu Asp Ala Val Leu Ala Leu Ile Glu Lys His Cys Asp Pro Ala His
 100 105 110
 Pro Ala Pro Leu Ala Gly Asn Ser Ile Ala Thr Asp Arg Ala Phe Ile
 115 120 125
 Arg Glu His Met Pro Arg Leu Asp Glu Ala Leu His Tyr Arg Met Val
 130 135 140
 Asp Val Ser Ser Val Lys Glu Leu Ala Arg Arg Trp Tyr Pro Arg Val
 145 150 155 160
 Tyr Tyr Lys Gln Pro Glu Lys Gly Leu Ala His Arg Ala Leu Ala Asp

61

	165	170	175
Ile Val Glu Ser Ile Arg Glu Leu Asp Tyr Tyr Arg Arg Ser Phe Phe			
	180	185	190
Val Ala Glu Pro Gly Pro Thr Ser Glu Gln Cys Ala Asp Asp Ala Gln			
	195	200	205
Ala Ala Val Asp Arg Phe Ala Pro Tyr Phe Asp			
	210	215	

<210> 431

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 431

ggaaacagta tgaccatg

18

<210> 432

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 432

gtaaaacgac ggccagt

17